

Supporting Online Material

Precise Manipulation of Chromosomes *in vivo* Enables Genome-wide Codon Replacement

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Materials & Methods

Strains and Culture Conditions

The λ -prophage was obtained from strain DY330 (1), modified to include the *bla* gene and introduced into wild-type MG1655 *E.coli* by P1 Transduction at the *bioA/bioB* gene locus and selected on ampicillin to yield the strain EcNR1 (λ -Red $^+$). Replacement of *mutS* with the chloramphenicol resistance gene (*chloramphenicol acetyl transferase, cmR*) in EcNR1 produced EcNR2 (*mutS* $^-$, λ -Red $^+$). EcNR2 was grown in low salt LB-min medium (10 g tryptone, 5 g yeast extract, 5 g NaCl in 1 L dH₂O) for optimal electroporation efficiency and compatibility with zeocin selection. EcNR2 was used as the ancestral strain for all recoded strains reported in this manuscript.

Oligonucleotides

All oligonucleotides were obtained from Integrated DNA Technologies. Oligonucleotides (Table S3) used in the MAGE process were designed according to the following specifications: 1) 90 nucleotides in length, 2) contain a single mutation to effect the TAG to TAA codon conversion, 3) two phosphorothioate linkages at both the 5' and 3' ends to attenuate exonuclease activity and to increase half life, 4) minimize secondary structure (ΔG threshold values, self-folding energy), 5) target lagging strand at the replication fork. No additional purification was used following oligonucleotide synthesis. Primers were purchased from IDT for the multiplex PCR assays and loci sequencing reactions (see description below and Tables S12 and S13).

MAGE-generated Codon Conversions

A single clone of the EcNR2 strain was grown in liquid cell culture, which was used to inoculate 32 separate cultures for parallel modification of all TAG codons. Modification of these codons was achieved through continuous MAGE (2) cycling. Each culture was grown at 30°C to mid-logarithmic growth (i.e., OD₆₀₀ of ~0.7) in a rotor drum at 200 RPM. To induce expression of the λ Red recombination proteins (Exo, Beta and Gam), cell cultures were shifted to a 42°C water bath with

vigorous shaking for 15 min and then immediately chilled on ice. In a 4°C environment, 1 mL of cell culture was centrifuged at 16,000x g for 30 seconds. Supernatant media was removed and cells were re-suspended in 1 mL dH₂O (Gibco cat# 15230). This wash process was repeated. Supernatant water was removed the pellet was resuspended in the appropriate pool of 10 oligos (1 uM per MAGE oligo in 50 uL dH₂O). The resuspended oligos/cell mixture was transferred to a pre-chilled 96-well, 2 mm gap electroporation plate (BTX, USA) and electroporated with a BTX electroporation system using the following parameters: 2.5 kV, 200 Ω, and 25 µF. The electroporated cells were immediately transferred to 3 mL of LB-min media for recovery. Recovery cultures were grown at 30 °C in a rotator drum for 2-2.5 hours. Once cells reached mid-logarithmic growth they proceeded to the next MAGE cycle. This approach introduces genomic modifications while allowing cells to evolve and adapt to those changes. Moreover, this approach is designed to explore extensive genotype and phenotype landscapes by creating combinatorial genomic variants that leverage the size of the cell population. After 18 MAGE cycles, cells from each population were isolated on LB-min agar plates. Forty-seven clones from each of the 32 cycled populations were selected and subjected to genotype and phenotype analyses. From each population the clone with the greatest number of modifications (an average of 8 modifications per clone) and minimal aberrant phenotypes (*i.e.*, auxotrophy, decreased fitness) was selected. Further MAGE cycles were employed (typically 6 cycles, but in some cases up to 15) to yield strains with complete sets of 10 targeted modifications.

Genotype Analyses

TAG-to-TAA codon conversions were analyzed using three main methods: 1) Multiplex allele-specific colony PCR (MASC-PCR), 2) Multiplex allele-specific colony quantitative PCR (MASC-qPCR) and 3) Sanger DNA sequencing.

Multiplex Allele Specific Colony PCR (MASC-PCR)

Based on previously described allele-specific PCR techniques, we developed the MASC-PCR method to test for TAG-to-TAA codon conversion in our recoded strains (the ancestral EcNR2 strain was the negative control). Three primers were designed for each locus: 1) a forward primer for the

TAG sequence, 2) a forward primer for the TAA sequence and 3) a reverse primer compatible with both forward primers (Table S12). Primers were designed for a target T_m of 62° C. The two forward primers were identical except that the most 3' nucleotide hybridized to produce either a GC base pair for the wildtype (TAG) codon or an AT base pair for the mutant (TAA) codon. Thus, every clone from each of the 32 populations was interrogated via two MASC-PCR reactions, in which each reaction assayed 10 different loci (with one set assaying four loci). One reaction assayed the wild type (TAG) sequence and a second reaction assayed the mutant (TAA) sequence, yielding two binary reactions that revealed the sequences of the targeted codons (Fig. S4). A clone containing the mutant allele generated PCR products only using the mutant allele primers and not the WT primers and vice versa for a clone with the wild-type allele. To minimize nonspecific amplification of MASC-PCR primers, a gradient PCR was performed to experimentally determine the optimal annealing temperature for each MASC-PCR primer pool (typically between 64 - 67° C). Multiple loci were queried in a single PCR reaction using the multiplex PCR mast2er mix kit from Qiagen. Each MASC-PCR primer set produced amplicon lengths of 100, 150, 200, 250, 300, 400, 500, 600, 700, or 850 bps, corresponding to up to 10 different genomic loci. We found that using a 1:100 dilution of saturated clonal culture in water as template generated the best MASC-PCR specificity. Typical 20 uL MASC-PCR reactions included 10 uL 2x Qiagen multiplex PCR master mix, 0.2 uM of each primer, and 1 uL of template. MASC-PCR cycles were conducted as follows: polymerase heat activation and cell lysis for 15 min at 95° C, denaturing for 30 sec at 94° C, annealing for 30 sec at experimentally determined optimal temperature (64-67° C), extension for 80 sec at 72°C, repeated cycling 26 times, and final extension for 5 min at 72°C. Gel electrophoresis on a 1.5% agarose gel (0.5x TBE) produced the best separation for a 10-plex MASC-PCR reaction. (See Fig. S4 for representative gel picture of MASC-PCR reaction.)

Multiplex allele-specific quantitative colony PCR (MASC-qPCR)

In complement to MASC-PCR analyses, we also developed a highly multiplexed quantitative PCR screen to rapidly identify highly modified clones (Fig. S3). Typical multiplexed qPCR reactions

employ multiple fluorescence and distinct detection events to assess multiple PCR reactions in one sample, and are generally limited by the available optics and fluorescence to 4 channels. Instead, we needed a robust, economical test that employed many different non-optimized primers, did not require more expensive fluorescently labeled oligos, and would work for 10-plex reactions. We accomplished these goals with SYBR Green I detection, which gauges the total amount of DNA produced in the reaction. Two qPCR reactions were compared for each clone evaluated, one with 10 pairs of primers matched to the unmodified TAG genes, and the other with 10 primer pairs matched to the intended TAA modifications. The TAG reactions were expected to proceed most efficiently with a wild-type template, and the TAA reactions most efficiently with a fully modified template. Intermediate values between these extremes also provided an effective, though nonlinear gauge of the extent of modification for each clone (Fig. S3 A-C).

Each colony was used as template for a pair of qPCR reactions comparing the amplification efficiency when matched to primers terminating in wild-type or targeted mutant sequence. The experimental measurement for a given clone is then compared to the equivalent values measured for the unmodified starting (negative control) strain. This reference value is subtracted from each ΔC_t to yield a $\Delta\Delta C_t$, with unmodified clones scoring close to zero (as with the negative control colonies). The largest $\Delta\Delta C_t$ values were expected to indicate the most modified clones, which we confirmed by genotyping clones with varying $\Delta\Delta C_t$ values (Fig. S3C) Large numbers of clones could be quickly assessed using this approach (up to 190 per 384-well plate, plus 2 negative controls). A typical assessment of MAGE-cycled clones comprised of 4 groups per plate, i.e. for each culture targeting 10 modifications, 2-4 control colonies and 44-46 queried colonies. After identification of the most promising clones, site-specific qPCR genotyping (Fig. S3D) was used to identify which specific sites had been modified, selecting the best clones for further modification.

Individual bacterial colonies were picked into 0.5 mL sterile distilled deionized water, with 5 μ L of this suspension used as template in 20 μ L qPCR reactions containing 1x NovaTaq buffer, 0.5 U NovaTaq Hotstart DNA Polymerase (EMD Biosciences), 250 μ M each dNTP, 0.5x SYBR Green I

(Invitrogen), and 5% DMSO. Primer concentrations were 50 nM for each primer (i.e. 500 nM total for 10 forward primers and 500 nM total for 10 reverse primers). A typical qPCR program included a 10 minute hot start at 95° C, followed by 40 cycles (95° C for 30 seconds, 60° C for 30 seconds, 72° C for 30 seconds) finishing with a melt curve analysis. All reactions were performed in a 7900 HT system (Applied Biosystems, Inc.). PCR primers for all sites were designed to have a melting temperature estimated at 62° C. Reverse primers were chosen to yield amplicons in the size range of 200-225 bp. No optimization was needed for qPCR primer sequences or for multiplex/singleplex reaction conditions.

Sanger Sequencing of 314 TAG to TAA loci

DNA sequencing was employed to confirm the results of the above PCR assays and to determine genotypes for 16 sites that gave ambiguous results by MASC-PCR. Amplicons 200-300 bp in length surrounding each of the 314 TAG sites were sequenced from the top-scoring clones by colony PCR as above. Sanger sequencing to confirm allelic replacements was performed by Agencourt Bioscience Corporation and the Biopolymer Facility in the Department of Genetics at Harvard Medical School. Mutations were identified by sequence alignment to the reference MG1655 genome.

Phenotype Analyses

To ensure that the codon replacements did not introduce any significant aberrant phenotypes, we conducted a number of experiments that assessed the fitness of the recoded strains. These experiments included measurements of: 1) strain growth rates, 2) auxotrophic rates and 3) frequency of recombination. Growth rate measurements were obtained by growing replicates of the recoded strains in LB-min media in 96-well plates at 30°C and obtaining OD₆₀₀ measurements using Molecular Devices plate readers (M5 and SpectraMax Plus). Auxotrophic rates were obtained by spotting all clonal isolates (1504) from the MAGE-cycled experiments on M9 minimal media plates (200 mL 5x M9 medium, 1 mL 1 M MgSO₄, 5 mL 40% glucose, 100 µL 0.5% vitamin B1 (thiamine), 1 mL D-biotin (0.25 mg/mL), up to 1 L water + 15g Agar). The recombination frequency of each isolate was obtained by

performing the allelic replacement protocol using a lacZ 90-mer oligo that produced a premature stop codon in the chromosomal *lacZ* gene. In general, 250-500 cells were plated on LB-min+Xgal/IPTG (USB Biochemicals) agar plates. Frequency of allelic replacement was calculated by dividing the number of white colonies by the total number of colonies on plates. All phenotypic results are reported in Table S6.

Hierarchical Conjugation Assembly Genome Engineering (CAGE)

Donor and recipient strains were grown in 3 mL LB-min containing the appropriate positive selectable antibiotics. Once cells reached logarithmic-saturated growth, 2 mL samples of each culture were transferred to 2 mL Eppendorf tubes. Cells were washed three times in order to remove antibiotics present in the growth cultures. The washing procedure consisted of centrifuging samples at 5000 rpm for 2 minutes at room temperature, removing the supernatant, and re-suspending the cell pellet in fresh LB-min containing no antibiotics. After the final wash, the donor and recipient pellets were concentrated in 100 μ L LB-min in order to enhance cell-cell contact during conjugation. Conjugation was initiated by combining 80 μ L of ~20x concentrated donor culture and 20 μ L of ~20x concentrated recipient culture. In order to minimize F pilus shearing, cells were gently mixed by pipetting. In order to minimize turbulence that can disrupt cell-cell contact during conjugation and to maximize genome transfer, the entire 100 μ L donor-recipient mixture was transferred as a series of 2 x 20 μ L and 6 x 10 μ L spots onto an LB-min agarose plate lacking antibiotics. This conjugation plate was incubated at 32° C for 0.5-2 hours, then the cells were re-suspended directly off of the plate using 1.5 mL LB-min and concentrated into a final volume of 250 μ L. Desired recombinant genomes were selected by inoculating 5 μ L of the concentrated post-conjugation culture into LB-min containing the correct combination of positive selection antibiotics (e.g., 10 μ g/mL zeocin, 95 μ g/mL spectinomycin, and 7.5 μ g/mL gentamycin). The conjugated cells that populated the selected culture were then subjected to a negative selection using either *tolC* or *galK* to ensure proper DNA transfer of TAA codons at critical junction points between donor and recipient cells (see Fig. 4).

This engineered conjugation method was tested for the first (1/32 genome, ~143 kb) and last (1/2 genome, ~2.3 Mb) chromosomal transfer steps in the hierarchical assembly experiment (Fig. 1). By selecting for different combinations of markers across the donor and recipient genomes and subsequent screening of specific genomic loci, recombinant clones were isolated that contained the transfer of half or full (otherwise unmodified) genomes at a frequency of $\sim 2.5 \times 10^6$ (from a population of $10^9\text{-}10^{10}$ cells), indicating the successful DNA transfer from an integrated *oriT* with episomal expression of conjugal factors. Equivalent frequencies were observed for full genome transfers.

Upon completion of the conjugation process, we also observed the anticipated loss of the *oriT-kan* cassette in the recombinant strain. This observation yields a subtle, yet very useful feature of our engineered conjugation system. By not inheriting the *oriT* sequence, the strains are positioned to proceed to a subsequent conjugation by a one-step integration of the *oriT-Kan* cassette in a new, targeted chromosomal locus (Fig. 4A).

Illumina Whole Genome Sequencing

We prepared a paired-end Illumina sequencing library for three 1/8 genome strains C21 (regions 17-20), C22 (21-24), and C23 (25-28) using barcoded Illumina adapters. The barcoded library was sequenced on one lane using an Illumina GAII.

1. Genome prep (Qiagen Genome Prep kit)
2. Sheared 5 µg of gDNA to target size = 200 bp using covaris (estimated median band size 250 bp)
3. PCR purified DNA (QIAquick PCR purification kit)
4. End repair (Epicentre End-it™ DNA End-Repair kit)

Component	Volume (1x)
DNA sample	35
10x End-Repair Buffer	10
1 mM dNTPs	10
End-Repair Enzyme mix	5

dH ₂ O	40
Total (μL)	100

Incubate at 25 C for 30 minutes

5. PCR purified DNA (QIAquick PCR purification kit)
6. A-tailing (NEB Klenow Fragment (3'->5' exo-))

Component	Volume (1x)
DNA sample	32
Klenow buffer	5
1 mM dATP	10
Klenow (3'->5' exo-)	3
Total (μL)	50

Incubate for 30 minutes at 37 C

7. PCR purified DNA (QIAquick PCR purification kit)
8. Adapter ligation (adapters complements of Morten Sommer)
 - a. C21: TopPE-1 barcode = **AGC**
 - b. C22.DO:T: TopPE-3 barcode = **CTA**
 - c. C23: TopPE-4 barcode = **TCT**

Component	Volume (1x)
DNA sample	31
Rapid ligase buffer (2x)	35
PE adapter (50 μM)	2
Enzymatics Rapid (T4) ligase	2

Incubated at 20 C for exactly 10 minutes in a thermocycler, then immediately added PBI for the PCR purification

9. PCR purification (Qiagen MinElute PCR purification kit)
10. Gel purified adapter-ligated sequencing libraries on 2% agarose gel in 0.5x TBE (cut 2 mm bands corresponding to approximately 225 bp) (Qiagen Gel Purification kit)
11. PCR amplified sequencing libraries (2x KAPA HiFi Ready Mix; 11 cycles)
 - a. Standard Illumina PE PCR Primers

Component	Volume (1x)
2X KAPA HiFi Ready Mix	25
PE_PCR-f	1
PE_PCR-r	1
dH2O	13
Template	4

Step	Temp	Time (min)
1	95	5:00
2	98	0:20
3	62	0:15
4	72	1:15
5	Go to step 2	11x
6	72	3:00
7	4	Forev

12. PCR purified (QIAquick PCR purification kit)
13. Validated sequencing library
 - a. Cloned Illumina libraries using Invitrogen TOPO ZeroBlunt II
 - b. Transformed into OneShot Top 10 electrocompetent cells
 - c. Genewiz sequenced insert (Sanger sequencing; Seq. primer = M13 forward (Invitrogen): GTAAAACGACGGCCAG)
14. Size-selected sequencing libraries for ~225 bp bands (E-Gel® SizeSelect™ gels)
15. PCR purified Illumina libraries (Qiagen MinElute)
16. Quantitated contents of C21, C22.DO:T, and C23 libraries
 - a. PAGE, Low DNA Mass Ladder (Invitrogen), and SYBR gold staining
 - b. Densitometry
17. Prepared sequencing library by adding all 3 components to a final concentration of 10 nM
18. Sample QC, Clustering, and sequencing performed by BPF
 - a. Standard Illumina PE Sequencing Primers

Genome Assembly and Sequence Analysis

Read Sorting and Processing

The raw Illumina reads in FASTQ format were preprocessed and sorted using the 6-bp barcodes in the paired end adaptors. Reads that contained anomalous barcodes were discarded. Reads containing any bases with a quality score of 2, also called the *Read Segment Quality Control Indicator* (based on *Illumina Quality Scores* by Tobia Man), were discarded at this step, but all other reads were kept. After preprocessing, all reads were exactly 34 base pairs long.

Reference-based Assembly

The expected FASTA sequence of the EcNR2 parent strain was assembled by manually modifying the FASTA sequence of E. coli K-12 strain MG1655 to reflect the removal of mutS and the insertion of the lambda prophage genome into the bioAB operon. Next, the preprocessed reads were sorted into separate files by pair group and the *Burrows-Wheeler Aligner* program (*BWA*) (3) was used to separately align the paired reads from each of the three strains to the expected EcNR2 FASTA sequence. The *sample* algorithm was used to align the reads. The distribution of insert sizes was inferred at runtime. During the read alignment step of *BWA*, (the *a/n* command), a value of 10 was used for the suboptimal alignment cutoff.

Indel and SNP Filtering

After alignment, the *SAMtools* package (4) was used to create and sort BAM files for the assemblies. From these BAM files we generated a set of raw SNPs and short indels with respect to this reference assembly. These were then filtered using several criteria. First, using the *varFilter* script within *SAMtools*, we removed SNPs where the root mean squared mapping quality was less than 10, and indels where the root mean squared mapping quality was less than 25. We fitted the read coverage of each assembly to a gamma distribution and used the 99.95th and 0.05th percentile cutoffs for minimum and maximum read depth, beyond which SNPs and indels were discarded. We also discarded SNPs within 3 base pairs of a gap, and SNPs that occurred more densely than three within one 10 base pair window.

Region Masking

We used custom scripts to further filter SNPs and indels by masking regions of poor assembly. We masked regions containing many truncated reads, many incorrect read pairings, many non-unique alignments, and regions with motifs known to be problematic in Illumina sequencing (GGCnG). We defined truncated read regions as those containing multiple incompletely mapped reads, separated by less than one read length, containing at least 4 truncated reads and having a number of truncated reads totaling at least one half of the length of the contiguous region in which they were found.

Regions with incorrect read pairings were defined using the following method. We found read pairs whose insert size was outside of the 99.9th and 0.1th percentile of a fitted normal distribution of mate pair distance. These reads were counted in a 34-bp rolling window. As a thresholding step we chose contiguous regions where 10 or more of these reads were found in one window length. Additionally included were contiguous regions where only one read in a pair could be mapped, and these were thresholded with a rolling window in a similar fashion, using a 6-read cutoff. As a final masking step, we removed SNPs stemming from the replacement of amber stop codons as well as SNPs and indels where surrounding context was GGCnC, as these regions are known to be hotspots for Illumina sequencing errors.

Annotation

After removing SNPs and indels in the masked regions as described above, we attempted to associate the remaining SNPs and indels with functional consequences. We used a modified version of *Ensembl's SNP Effect Predictor* software (5), and the *Ensembl Bacteria* database to find SNPs that occurred within genes. We further categorized these by synonymous and non-synonymous coding changes, frameshift mutations, premature stop mutations, mutations in the 5' and 3' UTRs, and mutations less than 100 base pairs upstream of a transcript start site (Fig. S8). Coordinates were lifted over from ECNR2 to MG1655 to permit annotation of the SNPs and indels. This resulted in C21, C22, and C23 having 4,5, and 5 mutations respectively having no corresponding liftover coordinates in ECNR2. These are referred to as the "unmappable" in Figure S8.

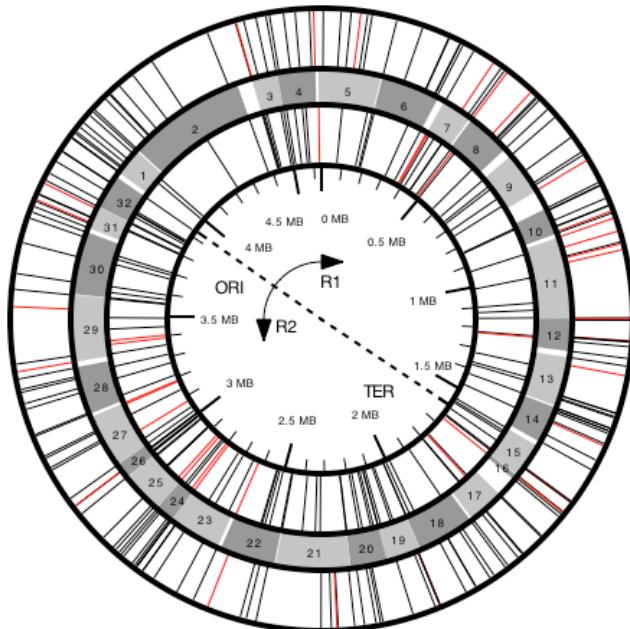


Figure S1. Circular representation of the *E. coli* genome depicting the coordinates and orientation of all TAG codons. TAG codons found in essential genes(6) are shown in red. The outer ring plots all clockwise transcribed TAG codons on the + DNA strand whereas the inner ring plots all counterclockwise transcribed TAG codons on the – DNA strand. The middle ring depicts the 32 sections of the genome targeted for TAG-to-TAA conversion. The inner circle plots the genomic coordinates, origin of replication (ORI), terminus (TER) and replicores 1 (R1) and 2 (R2).

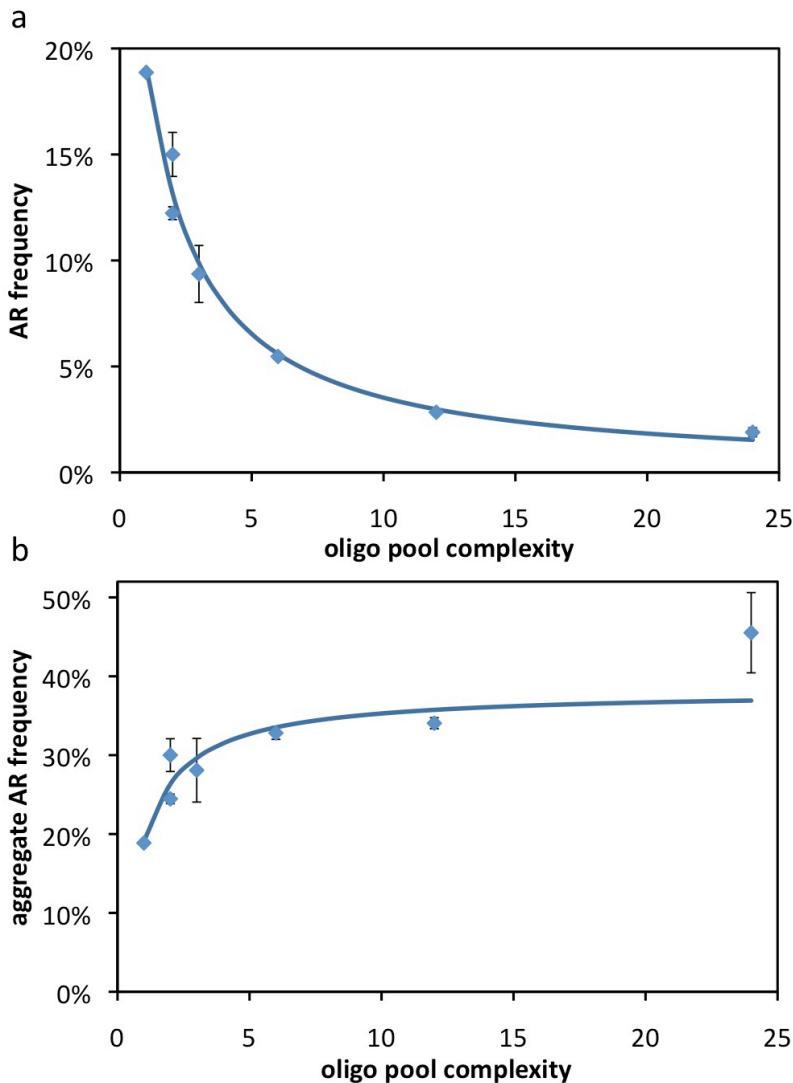


Figure S2. Multiplexing in MAGE leads to higher aggregate allele replacement (AR) frequencies. Multiplex oligo recombineering experiments were performed with equimolar oligo pools ranging in complexity from one to 24 oligos. AR frequencies were quantified for one conversion site corresponding to one oligo present in all pools. While individual AR frequencies (a) decrease as a function of higher complexity, the overall aggregate frequency (estimated as the product of individual frequency and pool complexity) (b) increases. Allele frequencies were measured using MASC-qPCR and curves are fit to the formula $y=a(1-e^{-b/x})$ for plot a and $y=ax(1-e^{-b/x})$ for plot b. Error bars indicate standard error ($n=2$).

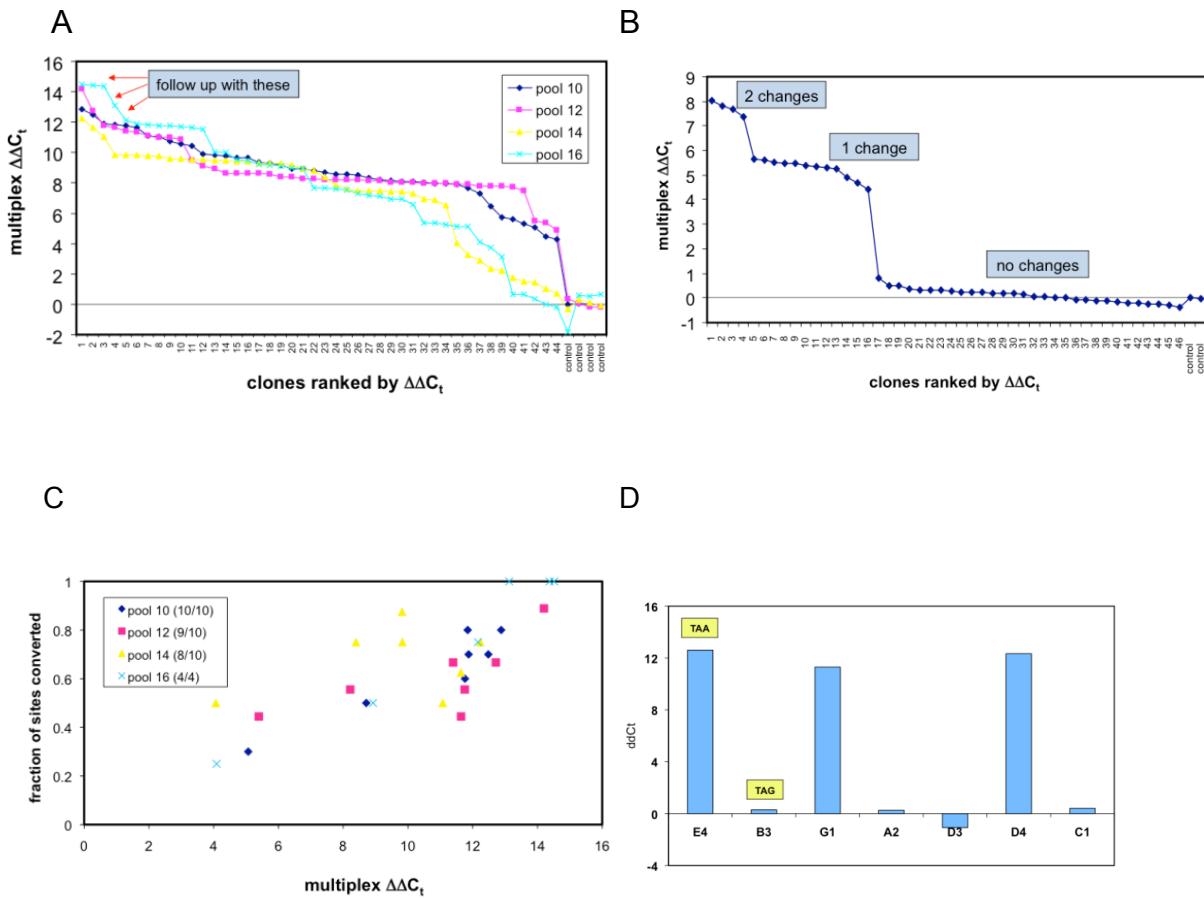


Figure S3. Multiplex allele-specific colony quantitative PCR (MASC-qPCR) to rapidly screen for the most modified clones. Multiplex reactions were used to determine which clones in the complex pool had been most highly modified. **A.** Clones from cultures receiving 18 cycles of MAGE processing (pools of 10 oligos) were sorted by their multiplex $\Delta\Delta C_t$ scores. Small numbers of top-scoring clones (typically 3–5) were then assessed at each TAG site of interest. **B.** When only two modifying oligos are used for allele replacement, multiplex $\Delta\Delta C_t$ values are more visibly clustered into groups representing 0, 1, or 2 modifications. **C.** Correlation between multiplex $\Delta\Delta C_t$ scores from (A) and the number of specific modifications achieved. The top multiplex $\Delta\Delta C_t$ -scoring clone was found to have the most allele conversions roughly 70% of the time. The legend indicates the number of modifications observed in the top-scoring clones. **D.** Singleplex reactions were used to genotype the most promising clones. Shown are 7 clones assayed at the tfaS stop codon, with singleplex $\Delta\Delta C_t$ values of 0.0 ± 0.7 for wild-type TAG and 12.1 ± 0.7 for modified TAA.

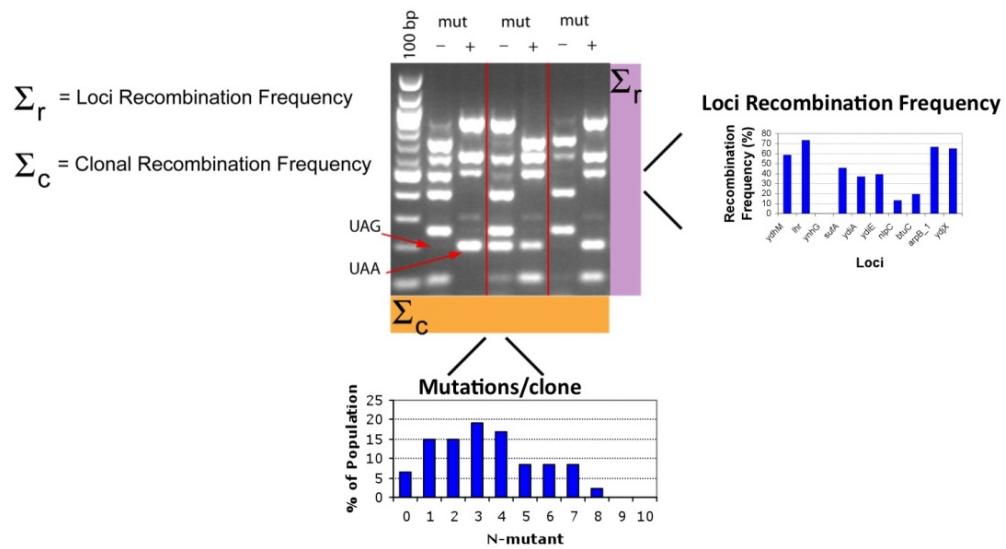


Figure S4. Multiplex allele-specific colony PCR (MASC-PCR) for the detection of codon conversions in each clone. The gel illustrates results from 3 MAGE-cycled clones. Ten sites are investigated in each lane where two MASC-PCRs are conducted for each clone: one reaction interrogates the TAG loci (-) and another reaction interrogates the TAA loci (+). Each reaction provides a binary output through the presence or absence of an amplicon band. Together, both TAG and TAA reactions provide sufficient information to determine the conversion status of a given codon. Summation of the rows of the 46 clones provides loci frequency data for each codon (plotted in Figure 2 in the main text). Summation of the columns of each clone provides a histogram of the mutations per clone (plotted in Fig. 3 in the main text).

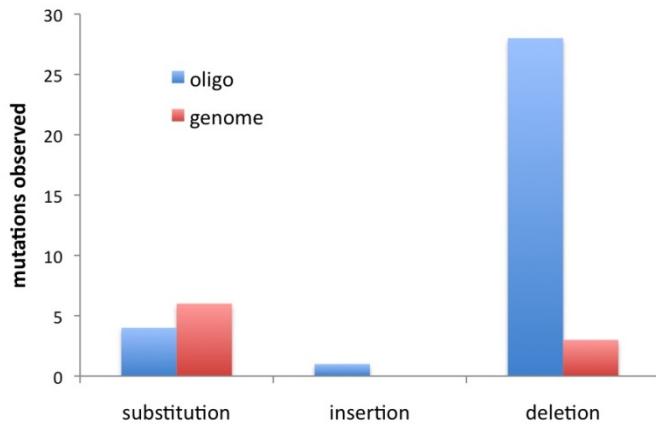


Figure S5. Off-target mutation in modified strains. From 96.3 kb of total Sanger sequencing, the majority of unwanted mutations were observed in regions corresponding to the annealing sites for the 90-mer oligonucleotides (blue). Sequenced mutations falling outside these 90 bp regions are shown in red. The principal error is a deletion, mostly single base deletions. These errors correspond to common defects arising from oligo synthesis.

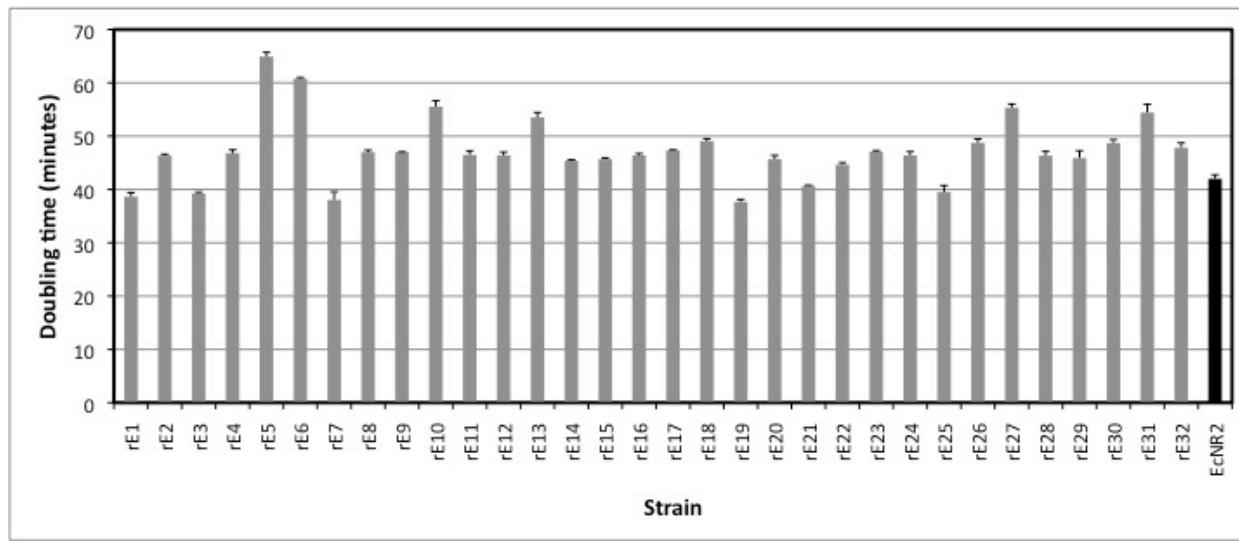


Figure S6. Individual growth rates of all 32 "top" recoded strains (10 out of 10 changes each, grey, rE1-rE32) following the successful replacement of all TAG-to-TAA codons versus that of the ancestral strain (black, EcNR2). A mix of increased and decreased growth rates was observed across the 32 strains with an average of 47 minutes/division. This is a mild decrease versus the growth rate (42 minutes/division) of the ancestral strain. Our parallelized MAGE approach across 32 strains allows us to easily identify strains with notable growth phenotypes (e.g., rE5, rE6). These strains can be investigated further to determine if these growth impediments are due to the codon changes or whether they arise from secondary mutations elsewhere in the genome

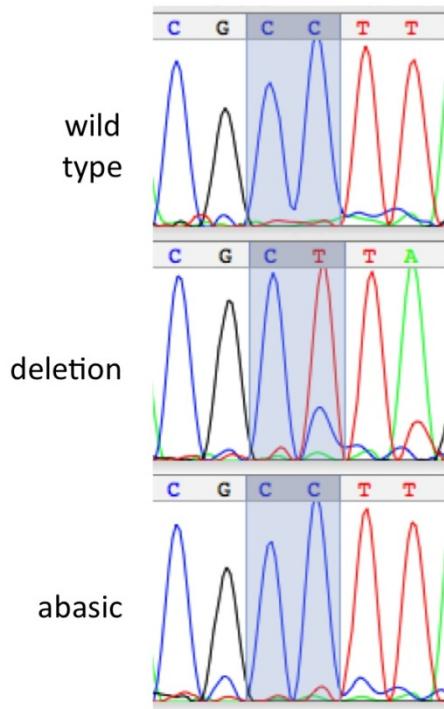
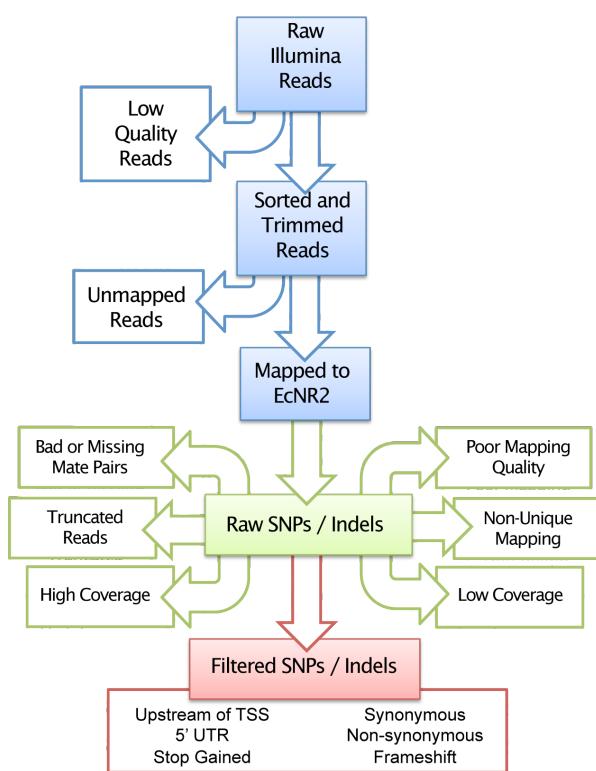


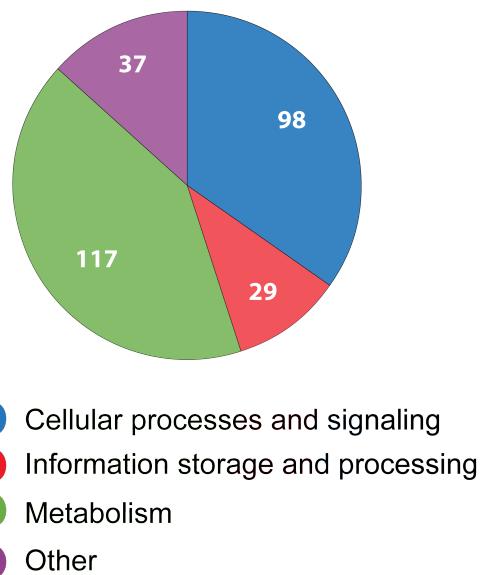
Figure S7. Some oligo defects can be fixed by host repair mechanisms. Oligos containing internal deletions are likely to result in equivalent mutations in the genome, but oligo synthesis chemistry can be optimized to minimize such deletions. In such cases, measures such as more aggressive deprotection and coupling conditions can then give rise to damaged oligos containing abasic sites. However, this second type of defect is readily repaired in the host. Three similar purified oligos were used to modify the selectable chromosomal *tolC* gene in separate cultures. An upstream modification (not shown) in each oligo creates a stop codon in *tolC*—selection against the *tolC* protein ensures only cells that have incorporated this oligo survive. PCR amplification of the resulting population and sequencing of this potentially heterogeneous product allows assessment of the effect of modifications at a second site. Top: only the initial stop codon was employed for this oligo, leaving the wild-type sequence C97-T102 of the *tolC* gene. Middle: this oligo coded for a deletion of C99, effectively shifting the subsequent peaks left one base position. However, a notable fraction (less than one-third) has not been shifted, indicating possible repair events (this fraction is very unlikely to arise from a defect in the oligo). Bottom: this oligo contained an abasic site at position 99, but the resulting population is almost completely wild-type, indicating likely cellular repair. These experiments were performed in strain EcNR2, which includes a deletion of the *mutS* mismatch repair gene.



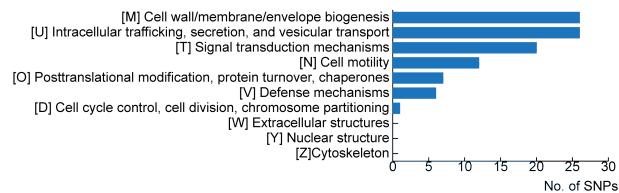
	C21	C22	C23	Total
Raw Reads	-	-	-	50,050,024
Low Quality Reads	-	-	-	10,049,324
Sorted and Trimmed	11,753,698	16,353,342	11,893,660	40,000,700
Unmapped Reads	448,348	506,335	413,368	1,368,051
Mapped to EcNR2	11,305,350 (96.19%)	15,847,007 (96.90%)	11,480,292 (96.52%)	38,632,64 (96.58%)
Raw SNPs / Indels	269	323	227	819
Poor Mapping Quality	108	148	75	331
Bad/Missing Mates	11	11	10	32
Truncated Reads	4	10	7	21
High Coverage	2	0	2	4
Low Coverage	3	5	3	11
Non-Unique Mapping	7	10	10	27
Filtered SNPs / Indels	110	128	102	340
Synonymous	29	33	24	86
Non-synonymous	50	46	41	137
Frameshift	11	11	10	32
Stop gained	2	4	2	8
5' UTR	2	3	3	8
Upstream of Transcript	2	4	1	7
Within Noncoding	2	8	4	14
Unmappable	4	5	5	14
No annotation	8	14	12	34

Figure S8. Bioinformatics sequencing analysis process and secondary mutation breakdown. We sequenced the entire genomes of three 1/8 recoded strains and identified off-target SNPs and short (1 bp) indels using BWA sequencing alignment (3). On-target TAG conversions are not included in this analysis. We found an average of 113 mutations/genome after each strain went through approximately 960 doublings, multiple lambda red inductions, and several conjugations. This corresponds to 2E-8 mutations/bp/doubling, which is consistent with the predicted basal mutation rate of the ancestral strain (EcNR2). These results indicate that MAGE and CAGE do not significantly compromise genome stability. Also see Fig. S9 and Tables S8-S11 for supporting data and information.

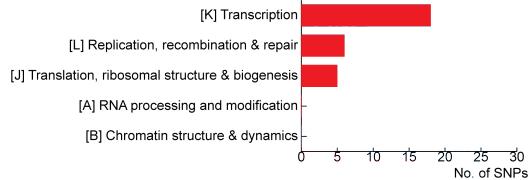
Functional annotation of all mutations



Cellular processes and signaling



Information storage and processing



Metabolism

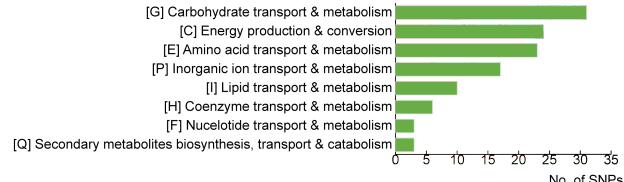


Figure S9 Functional annotation of all mutations as indicated by the COG category of the gene or regulatory region associated with the SNP or indel. Functional annotation of all mutations are summed across the three sequenced genomes. See Table S8 for complete list of secondary mutations.

Table S1. List of genes containing TAG codon and TAG genomic coordinate.

Genome Size = 4639675

Set	Gene	Essential	Direction	Gene.up	Gene.lo	Region.Size	TAG.coordinate
				3920623	3921005	383	
SIR.32.1	1 rbsB		0 forward	3934301	3935191	891	3935191
	1 rbsR		0 forward	3936250	3937242	993	3937242
	1 ilvL		0 forward	3948345	3948443	99	3948443
	1 ilvA		0 forward	3953354	3954898	1545	3954898
	1 wzzE		0 forward	3967054	3968100	1047	3968100
	1 aslB		0 forward	3980981	3982216	1236	3982216
	1 hemY		0 complemer	3984709	3985905	1197	3984709
	1 yigG		0 complemer	4000836	4001216	381	4000836
	1 recQ		0 forward	4003887	4005716	1830	4005716
	1 rmuC		0 forward	4015356	4016783	1428	4016783
SIR.1.2				4019889	4019968	80	
	2 tatD		0 forward	4021577	4022359	783	4022359
	2 yihL		0 forward	4058470	4059180	711	4059180
	2 yihW		0 forward	4072692	4073477	786	4073477
	2 yiiD		0 forward	4075472	4076461	990	4076461
	2 cpxP		0 forward	4103843	4104343	501	4104343
	2 frwD		0 forward	4145161	4145502	342	4145502
	2 zraR		0 forward	4201343	4202668	1326	4202668
	2 yjaB		0 complemer	4211703	4212146	444	4211703
	2 yjdK		0 forward	4350607	4350903	297	4350903
SIR.2.3	2 blc		0 complemer	4375212	4375745	534	4375212
				4417723	4417928	206	
	3 ulaf		0 forward	4421723	4422409	687	4422409
	3 yfY		0 complemer	4422539	4422814	276	4422539
	3 priB		1 forward	4423543	4423857	315	4423857
	3 ytfB		0 complemer	4426102	4426740	639	4426102
	3 ytfG		0 complemer	4431187	4432047	861	4431187
	3 msrA		0 complemer	4439561	4440199	639	4439561
	3 ytfN		0 forward	4442135	4445914	3780	4445914
	3 b4250		0 phantom gene	4472250	4472414	165	4472414
SIR.3.4	3 idnR		0 complemer	4488164	4489162	999	4488164
	3 b4273		0 forward, ins	4496618	4497523	906	4497523
				4497523	4497625	103	
	4 yjgX		0 complemer	4498066	4498512	447	4498066
	4 b4283		0 forward, ins	4505220	4505486	267	4505486
	4 fecE		0 complemer	4508713	4509480	768	4508713
	4 nanc		0 complemer	4536808	4537524	717	4536808
	4 fimB		0 forward	4538980	4539582	603	4539582
SIR.4.1	4 yjiN		0 complemer	4563989	4565269	1281	4563989
	4 yjiP		0 forward, yji	4567021	4567332	312	4567332
	4 mcrB		0 complemer	4575981	4577360	1380	4575981

	4 yjiQ	0 forward	4601500	4602225	726	4602225
	4 yjjV	1 forward	4611504	4612283	780	4612283
SIR.4.5		4612358	4612628		271	
	5 lplA	1 complemer	4621124	4622140	1017	4621124
	5 creC	0 forward	4634719	4636143	1425	4636143
	5 kefF	0 forward	47246	47776	531	47776
	5 yabI	0 forward	71351	72115	765	72115
	5 thiQ	0 complemer	72229	72927	699	72229
	5 murF	1 forward	94650	96008	1359	96008
	5 mutT	0 forward	111044	111433	390	111433
	5 pdhR	0 forward	122092	122856	765	122856
	5 sfsA	0 complemer	160782	161486	705	160782
SIR.5.6	5 btuF	0 complemer	177662	178462	801	177662
		182308	182445		138	
	6 cdaR	0 forward	182463	183620	1158	183620
	6 yael	0 complemer	184257	185069	813	184257
	6 yafl	0 forward	246712	247461	750	247461
	6 yagY	0 complemer	308582	309250	669	308582
	6 eaeH	0 forward	313581	314468	888	314468
	6 b0299	0 forward, ins	314811	315677	867	315677
	6 yahl	0 forward	343400	344215	816	344215
	6 yahM	0 forward	344628	344873	246	344873
SIR.6.7	6 prpE	0 forward	351930	353816	1887	353816
	6 cynR	0 complemer	357015	357914	900	357015
		374180	374608		429	
	7 frmR	1 complemer	378830	379105	276	378830
	7 b0361	0 forward, ins	380898	381803	906	381803
	7 yaiS	1 complemer	383283	383840	558	383283
	7 tra5_1	0 complemer	390963	391829	867	390963
	7 araj	0 complemer	410521	411705	1185	410521
	7 pgpA	1 forward	435813	436331	519	436331
	7 yajL	0 complemer	442275	442865	591	442275
SIR.7.8	7 panE	0 complemer	442828	443739	912	442828
	7 lon	0 forward	458112	460466	2355	460466
	7 mdIA	0 forward	468095	469867	1773	469867
		474460	474528		69	
	8 ybaA	1 forward	475896	476249	354	476249
	8 ybAJ	0 complemer	479558	479932	375	479558
	8 priC	1 complemer	489509	490036	528	489509
	8 aes	0 complemer	498238	499197	960	498238
	8 ybcF	1 forward	549662	550555	894	550555
	8 tra5_2	0 forward, ins	566361	567227	867	567227
SIR.8.9	8 ybCL	0 forward	570116	570667	552	570667
	8 rzpD	0 forward	577330	577791	462	577791
	8 ybcY	0 complemer	581375	582029	655	581375
	8 hoke	0 forward	607059	607211	153	607211
		608475	608607		133	
	9 ybdL	0 forward	632809	633969	1161	633969

	9 ybdM	0 complemer	633970	634599	630	633970
	9 rlpA	0 complemer	663325	664413	1089	663325
	9 ybeQ	0 complemer	674793	675770	978	674793
	9 ubiF	0 forward	694324	695499	1176	695499
	9 ybfH	0 compleme	715611	715820	210	715611
	9 ybfD	0 forward	737315	738076	762	738076
	9 nei	0 forward	745158	745949	792	745949
	9 abrB	0 complemer	745946	746992	1047	745946
	9 sucB	1 forward	760745	761962	1218	761962
SIR.9.10		769909	770318		410	
	10 bioD	0 forward	811493	812170	678	812170
	10 moaE	0 forward	818518	818970	453	818970
	10 ybhM	0 forward	820016	820729	714	820729
	10 ybhS	0 complemer	825342	826475	1134	825342
	10 ybiH	0 complemer	829195	829866	672	829195
	10 ybiR	0 forward	852870	853988	1119	853988
	10 yliD	0 forward, gs	871113	872024	912	872024
	10 yliE	0 forward	872202	874550	2349	874550
	10 ybjK	1 forward	886646	887182	537	887182
	10 rimK	0 forward	891190	892092	903	892092
SIR.10.11		892731	892782		52	
	11 ybjR	1 forward	904136	904966	831	904966
	11 cspd	0 complemer	921589	921813	225	921589
	11 lolA	1 forward	936595	937206	612	937206
	11 ycal	0 forward	963543	965807	2265	965807
	11 lpxK	1 forward	967589	968575	987	968575
	11 ycbK	1 forward	982298	982846	549	982846
	11 ycbX	0 complemer	1005714	1006823	1110	1005714
	11 tra5_3	0 complemer	1093498	1094364	867	1093498
	11 yceO	0 complemer	1118530	1118670	141	1118530
	11 yceF	0 complemer	1145234	1145818	585	1145234
SIR.11.12		1146763	1146844		82	
	12 plsX	0 forward	1146844	1147914	1071	1147914
	12 fabH	1 forward	1147982	1148935	954	1148935
	12 pabC	0 forward	1152523	1153332	810	1153332
	12 b1146	1 forward, yn	1202247	1202447	201	1202447
	12 ymfM	0 forward	1203045	1203383	339	1203383
	12 ymfR	0 forward	1204772	1204954	183	1204954
	12 tfaE	0 complemer	1207740	1208342	603	1207740
	12 ycgX	1 complemer	1211926	1212330	405	1211926
	12 ymgC	0 forward	1215971	1216219	249	1216219
	12 ycgY	0 forward	1244383	1244823	441	1244823
SIR.12.13		1255250	1255869		620	
	13 hemA	0 forward	1262937	1264193	1257	1264193
	13 b1228	1 forward, yc	1285932	1286207	276	1286207
	13 kch	0 complemer	1307040	1308293	1254	1307040
	13 sapB	0 complemer	1352529	1353494	966	1352529
	13 pspF	0 complemer	1364959	1365936	978	1364959

	13 ycjU	0 forward	1378172	1378831	660	1378831
	13 ycjV	0 forward	1378845	1379926	1082	1379926
	13 ycjG	0 forward	1386954	1387919	966	1387919
	13 ycjZ	0 forward	1390015	1390914	900	1390914
	13 intR	0 complemer	1410024	1411259	1236	1410024
SIR.13.14		1416328	1416497		170	
	14 sieB	0 forward	1416695	1417183	489	1417183
	14 b1354	0 forward (nc)	1417192	1417368	177	1417368
	14 ydA	0 forward	1423645	1424004	360	1424004
	14 b1367	0 forward	1417192	1417368	177	1417368
	14 tfaR	0 forward	1430435	1431010	576	1431010
	14 paaG	0 forward	1456288	1457076	789	1457076
	14 paaX	1 forward	1461563	1462513	951	1462513
	14 b1402	0 complemer	1465945	1466850	906	1465945
	14 ydCL	0 forward	1500481	1501149	669	1501149
	14 rhsE	0 forward	1525914	1527962	2049	1527962
SIR.14.15		1529675	1529765		91	
	15 yddJ	0 complemer	1542408	1542743	336	1542408
	15 ddpF	0 complemer	1555136	1556062	927	1555136
	15 yddV	0 complemer	1563782	1565164	1383	1563782
	15 ydEV	0 complemer	1596641	1598233	1593	1596641
	15 ydeA	0 forward	1615052	1616242	1191	1616242
	15 marA	1 forward	1617598	1617981	384	1617981
	15 marB	0 forward	1618013	1618231	219	1618231
	15 tfaQ	0 complemer	1632334	1632909	576	1632334
	15 ydfP	0 complemer	1637054	1637551	498	1637054
	15 rzpQ	0 forward	1646847	1647065	219	1647065
SIR.15.16		1647140	1647331		192	
	16 b1578	1 InsD, forwa	1648905	1649561	657	1649561
	16 ynFA	1 complemer	1653371	1653697	327	1653371
	16 speG	0 forward	1654208	1654768	561	1654768
	16 dmsD	0 forward	1662530	1663144	615	1663144
SIR.16.17		1676002	1676376		375	
	17 ydhM	0 forward	1724047	1724646	600	1724646
	17 lhr	0 forward	1727111	1731727	4617	1731727
	17 ynhG	0 complemer	1755745	1756749	1005	1755745
	17 sufA	1 complemer	1762042	1762410	369	1762042
	17 ydiA	0 forward	1785469	1786302	834	1786302
	17 ydiE	0 forward	1787637	1787828	192	1787828
	17 nlpC	0 complemer	1790291	1790755	465	1790291
	17 btuC	0 complemer	1792196	1793176	981	1792196
	17 arpB_1	0 forward	1801118	1801591	474	1801591
	17 ydjX	0 forward	1831425	1832135	711	1832135
SIR.17.18		1839427	1839513		87	
	18 nudG	0 forward	1839514	1839921	408	1839921
	18 b1788	0 complemer	1872102	1872206	105	1872102
	18 yeal	0 forward	1872376	1872822	447	1872822
	18 yeaX	0 forward	1883869	1884834	966	1884834

	18 yobB	0 forward	1923464	1924120	657	1924120
	18 exoX	0 forward	1924144	1924806	663	1924806
	18 yecN	0 forward	1950290	1950685	396	1950685
	18 otsA	0 complemer	1978212	1979636	1425	1978212
	18 dcyD	0 complemer	1996518	1997504	987	1996518
	18 yedM	0 complemer	2010025	2010375	351	2010025
SIR.18.19		2010450	2010649	200		
	19	0 complemer	2010724	2011038	315	2010724
	19 fliN	1 forward	2019112	2019525	414	2019525
	19 fliP	0 forward	2019893	2020630	738	2020630
	19 fliQ	0 forward	2020640	2020909	270	2020909
	19 yeds_1	0 forward	2032075	2032560	486	2032560
	19 cbl	0 complemer	2057988	2058938	951	2057988
	19 b1996	0 complemer	2066976	2067881	906	2066976
	19 hisL	0 forward	2088020	2088070	51	2088070
	19 wbbJ	0 complemer	2102518	2103108	591	2102518
	19 wcaM	0 complemer	2112526	2113920	1395	2112526
SIR.19.20		2113920	2113931	12		
	20 wcaL	0 complemer	2113931	2115151	1221	2113931
	20 wcaC	0 complemer	2128877	2130094	1218	2128877
	20 asmA	0 complemer	2137783	2139636	1854	2137783
	20 baeR	0 forward	2162300	2163022	723	2163022
	20 gatR_1	0 complemer	2169419	2169751	333	2169419
	20 tra5_4	0 forward, In:	2168556	2169422	867	2169422
	20 yegV	0 forward	2179118	2180083	966	2180083
	20 yegW	0 complemer	2180057	2180803	747	2180057
	20 yehQ	0 forward	2207122	2209122	2001	2209122
	20 yohC	0 complemer	2223066	2223653	588	2223066
SIR.20.21		2223728	2223748	21		
	21 yohF	0 complemer	2224531	2225292	762	2224531
	21 sanA	0 forward	2230900	2231619	720	2231619
	21 yejA	0 forward	2270386	2272200	1815	2272200
	21 yejE	1 forward	2273295	2274320	1026	2274320
	21 b2191	0 forward (nc)	2286927	2287049	123	2287049
	21 rcsD	0 forward	2311510	2314182	2673	2314182
	21 rcsC	0 complemer	2315049	2317898	2850	2315049
	21 yfaT	0 complemer	2332358	2332981	624	2332358
	21 menF	0 complemer	2377370	2378665	1296	2377370
	21 yfcO	0 complemer	2447250	2448071	822	2447250
SIR.21.22		2450358	2450378	21		
	22 yfcU	0 complemer	2450378	2453023	2646	2450378
	22 tfaS	0 forward	2468837	2469127	291	2469127
	22 yndl	0 forward	2492720	2492995	276	2492995
	22 yfdY	0 complemer	2493072	2493314	243	2493072
	22 yfeO	0 forward	2507652	2508908	1257	2508908
	22 mntH	0 complemer	2509490	2510728	1239	2509490
	22 xapR	0 complemer	2519615	2520499	885	2519615
	22 yfeR	0 complemer	2523952	2524878	927	2523952

	22 yffB	1 forward	2589269	2589625	357	2589625
	22 hda	1 complemer	2616097	2616843	747	2616097
SIR.22.23		2627035	2627237	203		
	23 yfgG	0 forward	2627312	2627503	192	2627503
	23 pbpc	0 complemer	2643035	2645347	2313	2643035
	23 yphA	0 forward	2671368	2671790	423	2671790
	23 yfhB	0 complemer	2695937	2696572	636	2695937
	23 kgtP	0 complemer	2722470	2723768	1299	2722470
	23 yfIA	0 forward, rai	2735176	2735517	342	2735517
	23 yfjQ	0 forward	2766687	2767508	822	2767508
	23 yfjR	0 forward	2767725	2768426	702	2768426
	23 ypjC	1 complemer	2781660	2783033	1374	2781660
SIR.23.24	23 ygaQ	0 forward	2784419	2786671	2253	2786671
		2784751	2784770	20		
	24 ygaR	0 forward	2784770	2785456	687	2785456
	24 yqAC	0 forward	2785664	2786260	597	2786260
	24 gabT	0 forward	2790757	2792037	1281	2792037
	24 ygau	1 complemer	2794359	2794808	450	2794359
	24 ygaM	0 forward	2798156	2798497	342	2798497
	24 luxS	0 complemer	2812240	2812755	516	2812240
	24 mltB	0 complemer	2822513	2823598	1086	2822513
	24 srlE	0 forward	2824414	2825373	960	2825373
SIR.24.25	24 norW	0 forward	2831934	2833067	1134	2833067
	24 ascB	0 forward	2839012	2840436	1425	2840436
		2840436	2840499	64		
	25 hycl	1 complemer	2840595	2841065	471	2840595
	25 hypB	0 forward	2849023	2849895	873	2849895
	25 ygbA	1 complemer	2854475	2854828	354	2854475
	25 pphB	0 forward	2857782	2858438	657	2858438
	25 ygcN	0 forward	2890679	2891950	1272	2891950
	25 mazF	0 complemer	2908778	2909113	336	2908778
	25 relA	0 complemer	2909439	2911673	2235	2909439
SIR.25.26	25 rumA	0 complemer	2911721	2913022	1302	2911721
	25 ppdc	0 complemer	2960463	2960786	324	2960463
	25 ptsP	0 complemer	2964210	2966456	2247	2964210
		2967074	2967277	204		
	26 mutH	0 forward	2967684	2968373	690	2968373
	26 ygeA	0 complemer	2977965	2978657	693	2977965
	26 kdul	0 complemer	2981310	2982146	837	2981310
	26 yqeF	0 complemer	2982433	2983614	1182	2982433
	26 ygel	0 forward	2991660	2991878	219	2991878
	26 pbl	1 forward	2991961	2992463	503	2992463
SIR.26.27	26 ygem	0 complemer	2993336	2993767	432	2993336
	26 b2860	0 complemer	2994394	2995299	906	2994394
	26 ygeP	0 complemer	2995711	2996010	300	2995711
	26 yqeC	0 complemer	3012309	3013079	771	3012309
		3013091	3013107	17		
	27 ygfJ	0 forward	3013182	3013760	579	3013760

	27 recJ	0 complemer	3034395	3036128	1734	3034395
	27 argO	1 complemer	3066195	3066830	636	3066195
	27 yggU	0 forward	3094405	3094695	291	3094695
	27 mutY	0 forward	3101035	3102087	1053	3102087
	27 glcC	0 forward	3126294	3127058	765	3127058
	27 yghQ	0 complemer	3129363	3130430	1068	3129363
	27 yght	0 forward	3132153	3132845	693	3132845
	27 ygiZ	1 complemer	3169901	3170233	333	3169901
	27 yqiB	1 complemer	3174880	3175302	423	3174880
SIR.27.28		3181420	3181760	341		
	28 b3045	0 forward, In:	3184532	3185437	906	3185437
	28 yqil	0 forward	3188654	3189718	1065	3189718
	28 ygiP	0 complemer	3203346	3204278	933	3203346
	28 yhaK	0 forward	3252341	3253042	702	3253042
	28 tdCA	0 complemer	3264149	3265087	939	3264149
	28 yhaC	0 forward	3266437	3267624	1188	3267624
	28 ecfH	0 forward, yr:	3294431	3295006	576	3295006
	28 yhbW	0 forward	3301470	3302477	1008	3302477
	28 nlpl	0 complemer	3306062	3306946	885	3306062
	28 dacB	0 forward	3326985	3328418	1434	3328418
SIR.28.29		3331548	3331657	110		
	29 ptsN	1 forward	3344600	3345091	492	3345091
	29 yhCC	0 complemer	3351143	3352072	930	3351143
	29 yhCE	0 forward	3363207	3364951	1745	3364951
	29 yhcO	1 complemer	3383879	3384151	273	3383879
	29 mreC	1 complemer	3396897	3398000	1104	3396897
	29 yhdN	0 complemer	3437163	3437531	369	3437163
	29 kefB	0 complemer	3476824	3478629	1806	3476824
	29 frID	1 forward	3501189	3501974	786	3501974
	29 bioH	0 complemer	3542096	3542866	771	3542096
	29 gntX	0 forward	3542904	3543587	684	3543587
SIR.29.30		3544296	3544352	57		
	30 malQ	0 complemer	3546008	3548092	2085	3546008
	30 glgA	0 complemer	3564623	3566056	1434	3564623
	30 yrhA	0 forward	3581064	3581477	414	3581477
	30 upgQ	0 complemer	3585393	3586136	744	3585393
	30 gadE	0 forward	3656389	3656916	528	3656916
	30 gadX	0 complemer	3663009	3663833	825	3663009
	30 yhjK	0 complemer	3681653	3683602	1950	3681653
	30 yhjR	0 complemer	3694020	3694208	189	3694020
	30 yiaG	0 forward	3717501	3717791	291	3717791
	30 xylR	0 forward	3733002	3734180	1179	3734180
SIR.30.31		3735275	3735445	171		
	31 sgbU	0 forward	3747255	3748115	861	3748115
	31 rhsA	0 forward	3760206	3764339	4134	3764339
	31 yibA	1 forward	3764360	3765202	843	3765202
	31 lctD	0 forward, lld	3777850	3779040	1191	3779040
	31 yibK	0 forward	3779238	3779711	474	3779711

	31 yibD	0 complemer	3787070	3788104	1035	3787070
	31 htrL	0 complemer	3790849	3791706	858	3790849
	31 coaD	1 forward	3807848	3808327	480	3808327
	31 rph	0 complemer	3813857	3814572	716	3813857
	31 dinD	0 forward	3815783	3816607	825	3816607
SIR.31.32		3816682	3816822	141		
	32 ligB	0 complemer	3817511	3819193	1683	3817511
	32 setC	0 forward	3834976	3836160	1185	3836160
	32 yicO	0 complemer	3840478	3841812	1335	3840478
	32 ivbL	0 complemer	3850913	3851011	99	3850913
	32 yidH	0 complemer	3853983	3854330	348	3853983
	32 glvC	0 complemer	3860010	3861626	1617	3860010
	32 yidS	0 forward, cb	3867400	3868464	1065	3868464
	32 yieH	0 forward	3894797	3895462	666	3895462
	32 yieJ	0 forward, cb	3896045	3896632	588	3896632
	32 atpE	0 complemer	3918973	3919212	240	3918973
SIR.32.1		3920623	3921005	383		

Table S2. List of genes containing TAG codons that overlap the open reading frame of a second gene.

TAG gene	overlaps the	of gene	coding change
abrB	tail	nei	silent*
aes	tail	hemH	silent
B1996	tail	yoeA	silent
B2860	head	ygeO	G6R
B3045	head	yqiG	G6R
bic	tail	sugE	silent
exoX	tail	ptrB	silent
frwD	tail	yijO	T280I
hypB	head	hypC	G4S
kgtP	tail	yfiM	silent
ligB	tail	yicG	silent
mdlA	head	mdlB	S3N
murF	head	mraY	V3I
nei	tail	abrB	silent*
nudG	tail	ynjH	T80I
paaX	head	paaY	D7N
panE	head	yajL	S13N
rbsR	tail	hsrA	S465F
sapB	head	sapC	S5N
sgbU	head	sgbE	E3K
tatD	tail	rfaH	silent
tfaE	tail	ymfS	P129L
tfaS	tail	yfdK	P138L
ugpQ	tail	yhhA	T143I
wbbJ	head	wbbK	V6I
wcaC	head	wcaD	S9N
ybjR	tail	ybjS	silent
ycbX	tail	ycbW	silent
ycjG	tail	mpaA	P255L
yeaL	tail	yeaM	T260I
yegV	tail	yegW	silent*
yegW	tail	yegV	silent*
ygcN	head	ygcO	A4T
ygeA	tail	lysR	A308V
yibD	tail	yibQ	A316V
yidH	head	yidG	S4N
yidS	tail	dgoT	silent
ytfB	tail	ytfA	S104F
zraR	tail	purD	silent

* two TAG-terminated genes overlap tails with terminal CTAG sequences
(converted to TTAA, all silent coding changes)

Table S3. List of oligonucleotide sequences for every TAG-to-TAA mutation

Region	Gene	Sequence of 90mer mutator oligonucleotides
1	rbsB	a*t*gacgtatTTatgtcaccatcaggtcatacaacCTgattaaaaTtactgcTTaacaaccAGTTcagatcaaccggatacttagcct*g*a
1	rbsR	g*a*aaacaaccgatggtaataattgtatcaaaagacagcgtaaatTtaaggccgaaccgcgttccatcagaatcggaGtaagtgtAATC*g*t
1	ilvL	c*g*gacTTTCGGTcGGGGTCTtagTCgttaaggCTgtatCTTcaaggCCGTtCCatcagaatcggtggataa*t*t
1	ilvA	c*a*caaAtgacgtgtcgccGGGTAGGCCTgataaAgcgaAGCGCTATCAGGCACTTTCCttaACCCGCCAAAAGAACCTGAACGCC*g*g
1	wzzE	c*t*tTCACATCGATTCTTCGAATAAGCGGCAGGCCTTCGCTCACCGCAGCAGTGTtTtattTCAGCAACGGCGGGTTAATG*c*g
1	asIB	g*g*cgttacGCCGcatCCGGcaatcaaccgcaggcggccgattttTacttactcaccaccAGCAAATGCGCATGcataatgtcgc*t*g
1	hemY	a*g*ctgcAGCTATCGTcGCAGCGTTGATGTTAACGTTGcAGATAACCCGCCACAGTAAttCCttCTCACCCGGAGGCAACGACCT*c*c
1	yigG	t*t*cagtatgctaAtgCTTGcACCTACTGATTcatcaaaACAATAAttatGGAGTATTATGAGTAAGGAATATATGAACGATGGTTCA*t*t
1	recQ	a*a*cgttacGGAGTCTTcATACTGGACTTTTATGCTGCTGAAttCTTCGTCATCGCCATCAACATGCGCACGAATCAGGCCA*t*a
1	rmuC	g*t*cgtatGCCCTAGATTCTACCCGGTTAACtACTCCAAATGGGTTAGCGCAGTGTGATTATATTcatCGCGTTGATAAGCTT*c*a
2	tatD	a*a*AGAGATTAAGCACAGTGTGAAGAAATACCGAGTCCGCAAAACTTaaaACGCAATCCAAACAGTGTtTGAATTAGCATCCGTGG*t*g
2	yihL	g*t*tgtAGATCTTCTTGCGTTATTATTGTcACCATAAAACACtTAACAGATTAGTGAAGGTCTACGGCCTCAAATGCCAATATT*c*a
2	yihW	g*g*cTATGTTGGCAAGGTATGAAGCCAGGTTACGGTcACAAAAATTTacGCGTCTCCTGGGGAAAGAATGATTCAATTGGCTGTCTT*g*t
2	yiiD	c*c*aaggACTAATATAATGACCTGAATGAGAGAGGGCAGCACGCCCTCTCCATCAgTtactCTTCGTTCCGCCCTTCATAC*g*g
2	cpxP	g*g*gaaAGACAGGGATGGTGTATGGCAAGGAAAACAGGGTTAAttCTGGAAACGTGAGTTGCTACTACTCAATAGCTCAACGATG*a*a
2	frwD	g*g*aatATGCCGGCAGTACCAcAGCCAActGACAGAAAAACCGAAttCTCAGAATAAGATGGTTGCTGCAGGCGCAGAAAGCAGT*t*g
2	zraR	t*a*tccACTGGGACGACTGTTCTGCCGGAAGAGATATCGGCTGGCGCgtATCGAACGCGAGCAGAAAttACGCGACAGTTGCAAT*a*g
2	yjAB	g*g*gaaACCGTATCCGTTGCTGAATCTGGCGTATGTGGGGCGTAAGCGATTtTCTCATCCGGTGGCTGAACtTCAGGTTAGTA*c*c
2	yjdK	t*t*AGAGAATAGTGCCTTATGTTCTTATCCTCTGGTtacttgtaAAActGACGGAAATAGTCAACTGTcATAATGT*t*g
2	blc	t*t*tgtAGTcAGTAAATTATTGGGTACAGCAGCCTGGTAGTTAAtGAGTGTcAGTTGAGGTTGCTGAGGATTGTCTCTTGT*t*g
3	ulaF	a*g*accAGTTATCTCCGAGGAAGGAAATTCCGcAGCGCGTtTtactCTGCCGTAATAAGCGTTAGGACCGTGTtACGcAtGA*a*g
3	yjfY	g*g*gAGTAACGGCAATATGACGCCAGCGCGGATATTATCGCTAACACAGGTATAACCAACGAAACATTGCCATAGTTGCTTGC*c*c
3	priB	t*g*aaACGGCAGAAACTGCGACGCGGAATAACGTGCCATATGGTtagtCTCCAGAAATCTGCTCGCAtGCAAA*c*c
3	ytFB	c*t*gTTcACCCGCCAGCCGGATGGCAGTTTATTCTGTcGCcGTTAAtGAAGGGTCAACCAAGCCAGCTAAGGATTGTCTCTTGT*t*g*a
3	ytfG	a*c*gTTAGCCAAAGCGTAAGCCATCTTTAATGTTAATAACTAAtTAATTAAAGTGGCATCCTCCGcAtCCTCTGTATAAtGACG*g*g
3	msrA	t*t*ACTGTGGAATTGGCGGAATTGGCGTCTGTCTGCCGCCAGCATAACGTTACGGGTACAAATGTAGTTGTTGATAAAGTGTCT*t*t
3	ytfN	g*c*cttGTTGTGGCGTAAACTGCCGTAGACAAATATTGcATTGTTaaaACTCGAActGATAGAGCAACATCCAGTGCCTGGTcACAC*c*a
3	b4250	a*t*ATCTGCGCGCCTTttaAtACCTCAACCAGGCACTCGCTtAccGGACGATCATCACGAAGAAATCGGCAAGCGGAATAGCT*t*c
3	idnR	a*c*tgtGACCTCGGGTATCAGATTATCACGGCAACACGCTTAAGTTATTTCTTCAATTACACGTATTCTTGTCCGGACGTTG*c*c
3	b4273	g*t*ataAAATATCCGTATTCAATCAGCACAAGGTGGATTGCCCTtatTTCCAGACATCTGTTATCActTAACCCATTACAAGCCC*g*c

7	pgpA	g*t*cgtaggattaaataagagtcgcggctgtatgagacgtgacaagcgtcacatcaggcatcggtgcacaaTtacgacagaataccca*g*c
7	yajL	g*g*cgtaaaaagccatgaagtggcatcacaactggatggcggcaggattataattattacgagtaAtgtcggtgcggcaaac*g*t
7	panE	a*g*tgaatatgagcgcacccgcactggcactgggttcgcctccccctggtaAtgaagagactgaagccgtcaccactatcgatctgctgttcgc*g*g
7	lon	a*g*cctgccagccctgtttattagtgcattttgcgcagggtcaTtatttgcaactgcataccagacggttcatttgca*g*c
7	mdlA	g*g*cgaaccgtacgctaacaggcgcttgcggccacagttggctaaaatcacgcacggccttcgcgatccggagcg*t*c
8	ybaA	t*t*tcttacgctggccgagcaacatttgcattttggctgcggcacgcgcacagccgtacgcacTtattcgatgatt*g*a
8	ybaJ	t*t*tgtcaatgcgacgaaagagaatcctcgagttatctgttaAaattattacaaccataggtagaagtatgtccggaaaacctta*a*c
8	priC	g*c*gctggaaaaaatcgaaaacaggtagcgcgttacccgctaAcaatggagagaatatgtcactggaaaatgcgcgtacgatgtc*a*a
8	aes	g*a*ggcttcgcgcacggcgtcagtttaccgcctcagttAcgatacgcggcaacaagattagccatcattcgatatgtccg*g*c
8	ybcF	a*c*gcgtcaagcgtcgcatcaggcacaatgtctaattgcctacgaTtacagcgaatacaggccccgttcgcggcagcgtctt*c*a
8	tra5_2	t*g*atttatgctgggtgatccctacccacgtaatatggacacaggcTtaagcgaggttctgtttcaaattgttccggactgaggccgc*c*a
8	ybcL	t*c*gatcttaagtttagtcttacctcttgcagcatactctcaccTtactttatctcataaactgggttatctcagcgttgcgattt*t*a
8	rzpD	t*t*gctcaaaataattgcatgagttgcgcacatcgatatggtcagctTtattctgcactgcctattaatataacttctgggttccttcagtt*g*t
8	ybcY	a*a*aaccaagggtcaaggtaactgttagtaatgtttccgcaggaaaaataAcatccaaaccgcagcatgttctgccttaagacgtg*c*t
8	hokE	t*a*aatcatatcaggcgtaataccacaacccttaagtttagcgcctatggattactcccgacacggTtacttctcggtcgtaaag*c*g
9	ybdL	c*t*gaagcaaattaacggcctgcaagagtgtttgcgcaccgtcaatattccgcgcctggacggtaatagTtaaagctggcgcagg*c*g
9	ybdM	t*g*aagcaaattaacggcctgcaagagttgtttgcgcaccgtcaatattccgcgcctggacggtaataActaaagctggcgcagg*c*t
9	rlpA	c*a*aacccaaaggccattacagtcatattactaccgcgcagtaAcgtaaagcaggcatctgatgttcaatttctgttaatgcgtt*a*a
9	ybeQ	c*a*tccggaaccagagatgtcagtcaggaaattcgtgagactgaagattactgttaAagataaaaacaaggccggaaatttcattcg*g*c
9	ubiF	c*g*tcttatccgacctacggtggcacgcacccgcataatgtttaaggTtacaaccctaacgcataattcagcgcctgcgttcaaca*c*g
9	ybfH	c*a*ccgatgggtgcgttgcattatggctccggaggctgtgattgataatggtaAttacgcatacgaggatctgttgcaccccggtt*g*c
9	ybfd	c*g*caaggactgacgtcaggtagttctaaaccatagctgcctttTtattcaaacgtgaaatcaataagctcatcaggacatgcacaa*c*a
9	nei	t*g*ccatgcgcgttatttcaacctatgcgcgaagcggcggcTtagtgtgcagccaggcaccagtaaaacggcgcagatgac*a*g
9	abrB	t*g*acagggcctgcattgcgcgttatttcaacctatgcgcgaagcggcggcAtgtcggtgcagccaggcaccagtaaaacgg*g*c
9	sucB	g*a*taatgccttatccggctacagtgcaggtaaactaaactTtacacgtccagcagcgcgtcgatctccagcaactctt*t*g
10	bioD	t*c*gaagacgcgatctcgctcgcaatttaccaaatacagaatggTtacaacaaggcaaggttattgtacttccgttgcgcatttt*c*t
10	moaE	c*g*taaacgtatgtactgagcggtaaattgcgcgcacgcacgggtgccttatccgcctaacaaaaaaaTtaccagcgtttgcgcctgc*t*g
10	ybhM	g*c*gatgtgaagtttagttaagttcttagtgcattacggTtaatgaaaaaaacgcgtatgccttgcgcagacaagcgttata*g*c*t
10	ybhS	t*t*tatccgcctgcgtggctgaaaacccaaacgtcggctggattAggagaagagcatgttcatgccttatggacgttaatccgcacaa*g*a
10	ybiH	c*a*tatcgacctgatccgcaggattatgcacaaaggagttgtatgcgtatccgcgttgcgttgcgttaggtact*t*g
10	ybiR	t*c*tgaattatctcaaaaacttaaagcaaaaaggcggactcataatccgccttttatttgcgcagaccTtagtgtgcgggagttaa*c*t
10	yliD	t*t*tcctgtgaggtgattacccttcaagcaatattcaaacgttaatgcgttgcgcgttgcgttgcgttaggtact*g*c
10	yliE	g*a*ctgactgtaagtacgaacttattgattctggacatacgtaaaTtactctttactaatttccactttatccaggcggagaatg*g*c
10	ybjK	t*c*ggccaagggttgcgtgggtttttgttatctaaaacttacgttgcacccctctcaaccatcctcaaaaatctccgcgcg*a*t
10	rimK	c*g*caaaaacgcgcaggcaaaaccatgatcgttaatgtgattgcgatTtaaccacccgtttcaggcaatattctgtcgtagcgtggcggtt*c*g

32 yidS g*a*ttagcgcagtgggtggcacatattccacagttgaaggattaAccaacgcgcttcacatcgcccaccagcaggatataagagagc*g*c
32 yieH t*t*acctgaactgtggaaagcgcgtggatattacggcataAttcttcacactcccttcaacttacccgccttaattggcgctca*a*a
32 yieJ t*g*tctccactgcggcaagctgagactgtgggtgatttcgtaAttatttaataatgagaacaggccggagcgttaattcacacatc*c*g
32 atpE t*a*gttaacgttctgatattgctcttaaaaagcaacgcctaTtacgcgacagcgaacatcacgtacagacccagacctacagcga*t*c

Table S4. Frequency of TAG codon conversions at each locus

Region	Gene	Frequency of Codon Conversions
1	rbsB	39.1
1	rbsR	71.1
1	ilvL	41.3
1	ilvA	37.2
1	wzzE	29.8
1	aslB	20.5
1	hemY	37.2
1	yigG	51.2
1	recQ	39.5
1	rmuC	28.9
2	tatD	29.3
2	yihL	72.5
2	yihW	68.3
2	yiiD	42.5
2	cpxP	55.0
2	frwD	52.5
2	zraR	
2	yjaB	57.5
2	yjdK	10.3
2	blc	48.6
3	ulaF	43.5
3	yjfY	47.2
3	priB	45.5
3	ytfB	45.7
3	ytfG	51.1
3	msrA	40.9
3	ytfN	40.5
3	b4250	46.5
3	idnR	37.8
3	b4273	39.0
4	yjgX	23.8
4	b4283	34.1
4	fecE	37.2
4	nanC	15.4
4	fimB	
4	yjiN	27.3

4	yjiP	27.9
4	mcrB	94.9
4	yjjQ	22.0
4	yjjV	
5	IplA	48.9
5	creC	25.6
5	kefF	32.5
5	yabI	26.2
5	thiQ	14.6
5	murF	57.5
5	mutT	15.6
5	pdhR	32.6
5	sfsA	51.2
5	btuF	11.4
6	cdaR	51.2
6	yaeI	72.7
6	yafL	29.3
6	yagY	
6	eaeH	15.9
6	b0299	34.9
6	yahL	73.3
6	yahM	53.3
6	prpE	20.0
6	cynR	79.3
7	frmR	47.4
7	b0361	60.5
7	yaiS	54.8
7	tra5_1	37.8
7	araJ	25.5
7	pgpA	21.3
7	yajL	42.2
7	panE	36.2
7	lon	35.9
7	mdlA	27.7
8	ybaA	14.3
8	ybaJ	57.4
8	priC	66.0
8	aes	13.3
8	ybcF	34.8
8	tra5_2	15.2
8	ybcL	90.9
8	rzpD	44.2
8	ybcY	18.2

8	hokE	19.6
9	ybdL	14.3
9	ybdM	11.1
9	rlpA	6.8
9	ybeQ	55.3
9	ubiF	13.3
9	ybfH	12.2
9	ybfD	25.6
9	nei	31.9
9	abrB	51.5
9	sucB	26.7
10	bioD	22.7
10	moaE	52.5
10	ybhM	46.5
10	ybhS	33.3
10	ybiH	52.6
10	ybiR	17.4
10	yliD	38.9
10	yliE	44.4
10	ybjK	58.5
10	rimK	68.3
11	ybjR	21.1
11	cspD	33.3
11	lolA	10.3
11	ycaI	46.3
11	lpxK	50.0
11	ycbK	43.9
11	ycbX	22.5
11	tra5_3	34.2
11	yceO	64.3
11	yceF	
12	plsX	83.0
12	fabH	21.3
12	pabC	89.1
12	b1146	12.8
12	ymfM	78.7
12	ymfR	25.5
12	tfaE	
12	ycgX	
12	ymgC	89.4
12	ycgY	
13	hemA	34.1
13	b1228	6.1

13	kch	18.9
13	sapB	2.2
13	pspF	4.4
13	ycjU	10.9
13	ycjV	2.3
13	ycjG	4.4
13	ycjZ	9.8
13	intR	
14	sieB	31.9
14	b1354	28.3
14	ydaY	6.4
14	b1367	
14	tfaR	33.3
14	paaG	8.7
14	paaX	7.1
14	b1402	13.0
14	ydcL	2.1
14	rhsE	33.3
15	yddJ	37.8
15	ddpF	37.8
15	yddV	45.0
15	ydeV	31.0
15	ydeA	10.9
15	marA	33.3
15	marB	41.9
15	tfaQ	45.5
15	ydfP	
15	rzpQ	46.7
16	b1578	45.9
16	ynfA	42.6
16	speG	50.0
16	dmsD	40.4
17	ydhM	60.0
17	lhr	73.3
17	ynhG	
17	sufA	47.7
17	ydiA	37.8
17	ydiE	43.9
17	nlpC	13.3
17	btuC	22.0
17	arpB_1	69.8
17	ydjX	64.9
18	nudG	64.3

	b1788	35.6
18	yeaL	15.6
18	yeaX	17.8
18	yobB	31.1
18	exoX	14.7
18	yecN	56.5
18	otsA	28.9
18	dcyD	10.9
18	yedM	32.6
19	fliE	34.8
19	fliN	25.5
19	fliP	47.8
19	fliQ	34.1
19	yedS_1	45.5
19	cbl	31.9
19	b1996	32.6
19	hisL	42.2
19	wbbJ	62.8
19	wcaM	47.4
20	wcaL	17.0
20	wcaC	45.7
20	asmA	20.0
20	baeR	21.7
20	gatR_1	36.2
20	tra5_4	17.8
20	yegV	28.3
20	yegW	17.4
20	yehQ	38.3
20	yohC	70.2
21	yohF	33.3
21	sanA	85.2
21	yejA	25.0
21	yejE	33.3
21	b2191	21.1
21	rcsD	34.9
21	rcsC	26.8
21	yfaT	50.0
21	menF	70.0
21	yfcO	2.9
22	yfcU	21.7
22	tfaS	29.8
22	YPD1	23.4
22	yfdY	21.7

22	yfeO	48.9	
22	mntH	14.9	
22	xapR	8.7	
22	yfeR	23.4	
22	yffB	41.3	
22	hda	23.4	
23	yfgG	6.8	
23	pbpC		
23	yphA	17.0	
23	yfhB	27.7	
23	kgtP	38.3	
23	yfiA	22.7	
23	yfjQ	38.6	
23	yfjR	17.0	
23	ypjC	26.5	
23	ygaQ	40.9	
24	ygaR	57.1	
24	yqaC	40.0	
24	gabT	22.0	
24	ygaU	37.2	
24	ygaM	20.9	
24	luxS	30.2	
24	mltB	36.4	
24	srlE	43.9	
24	norW	14.6	
24	ascB		
25	hycI	19.4	
25	hypB	45.7	
25	ygbA	15.9	
25	pphB	61.4	
25	ygcN	24.4	
25	mazF	73.3	
25	relA	19.1	
25	rumA	44.7	
25	ppdC	35.1	
25	ptsP	14.7	
26	mutH	27.7	
26	ygeA	23.4	
26	kduI	39.1	
26	yqeF	17.8	
26	ygeI	39.1	
26	pbl	23.9	
26	ygeM	58.5	

	b2860	23.9
26	ygeP	27.7
26	yqeC	12.8
27	ygfJ	71.1
27	recJ	34.0
27	argO	43.2
27	yggU	41.3
27	mutY	65.2
27	glcC	56.5
27	yghQ	42.6
27	yghT	31.9
27	ygiZ	15.2
27	yqiB	21.1
28	b3045	26.7
28	yqiI	10.9
28	ygiP	26.7
28	yhaK	47.8
28	tdcA	78.3
28	yhaC	68.9
28	ecfH	19.6
28	yhbW	34.8
28	nlpI	82.9
28	dacB	19.6
29	ptsN	40.0
29	yhcC	34.1
29	yhcE	24.4
29	yhcO	66.7
29	mreC	20.0
29	yhdN	18.6
29	kefB	33.3
29	frlD	33.3
29	bioH	33.3
29	gntX	40.9
30	malQ	18.2
30	glgA	51.1
30	yrhA	0.0
30	ugpQ	67.4
30	gadE	69.0
30	gadX	29.5
30	yhjK	59.1
30	yhjR	23.4
30	yiaG	28.6
30	xyIR	

31	sgbU	37.0
31	rhsA	74.3
31	yibA	36.4
31	lctD	17.0
31	yibK	59.6
31	yibD	35.7
31	htrL	23.3
31	coaD	19.6
31	rph	53.5
31	dinD	
32	ligB	59.6
32	setC	51.6
32	yicO	70.2
32	ivbL	21.4
32	yidH	51.1
32	glvC	61.7
32	yidS	48.9
32	yieH	65.2
32	yieJ	56.5
32	atpE	24.2

Table S5. Frequency of TAG codon conversions.

TAG Gene Subset	# Codons Assayed	Allelic Replacement Frequency
All TAG genes	298/314	36.6% +/-19%
TAG transcript in + transcription direction	169/177	36.5% +/-19%
TAG transcript in - transcription direction	129/137	36.6% +/-19%
Essential genes with TAG	41/43	35.3% +/-19%
TAG codons overlapping 2nd reading frame	37/39	33.7% +/-19%

Frequency of allelic replacement is tabulated for: 1) all TAG codons, 2) TAG codons broken down by direction (+/-) of transcription, 3) essential genes that contain TAG codons, 4) TAG codons overlapping the reading frame of a second gene. The number of codons assayed is represented as a fraction of the number of successful masPCR reactions over the total number of genes.

Table S6. Properties of MAGE-cycled Strains

Strain Measurement	Ancestral EcNR2 Strain	Average of 32 TAG-to-TAA recoded strains
Growth Rates (30C)	42'	47'(+/-6)
Recombination Efficiencies	23%	21.6%(+/-2.5%)
Auxotrophic Rates	-	2.8%

Table S7. Five-stage hierarchical conjugation process

Stage	No. of Strains	No. of Conjugations	Average Size of Genomic Transfer	Strain Numbers
1	32	16	143 kb	rEc1-rEc32
2	16	8	267 kb	C1-C16
3	8	4	575 kb	C17-C24
4	4	2	1.15 MB	C25-C28
5	2	1	2.3 MB	C29-C31

Table S8. List and annotation of all secondary mutations

Strain	Feature	Start	End	WT	Mutant	Gene	Consequence	AA Change	COG	Type	Product
C21	snp	2055	2055	C	T	thrA	SYNONYMOUS_CODING	H	COG0527	E	fused aspartokinase I and homoserine dehydrogenase I
C21	snp	66039	66039	T	C	araD	NON_SYNONYMOUS_CODING	H/R	COG0235	G	L-ribulose-5-phosphate 4-epimerase
C21	snp	71695	71695	C	T	yabI	SYNONYMOUS_CODING	V	COG0586	S	inner membrane protein, SNARE_assoc family
C21	snp	76786	76786	A	G	sgrR	NON_SYNONYMOUS_CODING	W/R	COG4533	R	transcriptional DNA-binding transcriptional activator of sgrS sRNA
C21	snp	151352	151352	A	G	yadK	NON_SYNONYMOUS_CODING	V/A	COG3539	NU	predicted fimbrial-like adhesin protein
C21	snp	160383	160383	G	A	dksA	SYNONYMOUS_CODING	D	COG1734	T	DNA-binding transcriptional regulator of rRNA transcription, DnaK suppressor protein
C21	snp	195795	195795	C	T	cdsA	NON_SYNONYMOUS_CODING	A/V	COG0575	I	CDP-diglyceride synthase
C21	snp	332913	332913	C	T	yahB	NON_SYNONYMOUS_CODING	V/I	COG0583	K	predicted DNA-bindng transcriptional regulator
C21	indel	342758	342758	G	-	yahK	FRAMESHIFT_CODING	-	COG1064	R	predicted oxidoreductase, Zn-dependent and NAD(P)-binding
C21	snp	444898	444898	C	T	yajR	SYNONYMOUS_CODING	S	COG2814	G	predicted transporter
C21	snp	547694	547694	A	G	ylbE	SYNONYMOUS_CODING	E	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	indel	547831	547832	-	G	ylbE	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	658193	658193	A	G	tatE	SYNONYMOUS_CODING	K	-	-	TatABCE protein translocation system subunit
C21	snp	760107	760107	C	T	sucA	NON_SYNONYMOUS_CODING	P/S	COG0567	C	2-oxoglutarate decarboxylase, thiamin-requiring
C21	snp	804520	804520	G	A	ybhJ	NON_SYNONYMOUS_CODING	A/T	COG1048	C	predicted hydratase
C21	snp	822574	822574	T	C	ybhO	NON_SYNONYMOUS_CODING	N/S	COG1502	I	cardiolipin synthase 2
C21	snp	827752	827752	A	G	ybhF	SYNONYMOUS_CODING	C	COG1131	V	fused predicted transporter subunits of ABC superfamily: ATP-binding components
C21	snp	853211	853211	A	G	ybiR	SYNONYMOUS_CODING	R	COG0471	P	predicted transporter

C21	indel	883564	883564	G	-	cmr	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	987651	987651	G	A	asnS	SYNONYMOUS_CODING	N	COG0017	J	asparaginyl tRNA synthetase
C21	snp	995889	995889	A	G	ssuA	SYNONYMOUS_CODING	A	COG0715	P	putative aliphatic sulfonate binding protein
C21	snp	1005546	1005546	C	T	ycbW	SYNONYMOUS_CODING	V	-	-	predicted protein
C21	snp	1056395	1056395	A	G	torT	SYNONYMOUS_CODING	P	COG1879	G	periplasmic sensory protein associated with the TorRS two-component regulatory system
C21	indel	1093083	1093084	-	G	ycdT	FRAMESHIFT_CODING	-	COG3706	T	diguanylate cyclase
C21	snp	1110049	1110049	A	G	mdoG	NON_SYNONYMOUS_CODING	T/A	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	1146795	1146795	A	G	plsX	UPSTREAM (-49)	-	COG0416	I	probable phosphate acyltransferase
C21	snp	1241046	1241046	A	G	cvrA	SYNONYMOUS_CODING	S	COG3263	P	predicted cation/proton antiporter
C21	snp	1284157	1284157	A	G	narH	NON_SYNONYMOUS_CODING	Y/C	COG1140	C	nitrate reductase 1, beta (Fe-S) subunit
C21	snp	1456641	1456641	A	G	paaG	SYNONYMOUS_CODING	A	COG1024	I	predicted enoyl-CoA hydratase
C21	snp	1493717	1493717	A	G	ydcJ	NON_SYNONYMOUS_CODING	I/V	COG5383	S	predicted metalloenzyme
C21	snp	1513952	1513952	T	C	ydcW	SYNONYMOUS_CODING	C	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	1537774	1537774	G	A	narZ	SYNONYMOUS_CODING	T	COG5013	C	nitrate reductase 2 (NRZ), alpha subunit
C21	snp	1562401	1562401	T	C	dos	NON_SYNONYMOUS_CODING	T/A	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	1657766	1657766	G	A	ynfE	STOP_GAINED	W/*	COG0243	C	probable selenate reductase, periplasmic
C21	snp	1693853	1693853	G	A	uidA	SYNONYMOUS_CODING	G	COG3250	G	beta-D-glucuronidase
C21	snp	1753006	1753006	C	T	ydhZ	NON_SYNONYMOUS_CODING	E/K	-	-	predicted protein
C21	snp	1837592	1837592	G	A	ynjE	SYNONYMOUS_CODING	Q	COG2897	P	predicted thiosulfate sulfur transferase
C21	indel	1866698	1866698	C	-	yeaG	FRAMESHIFT_CODING	-	COG2766	T	protein kinase, function unknown; autokinase
C21	indel	1950710	1950710	C	-	cmoA	UPSTREAM (-16)	-	COG2226	H	tRNA cmo(5)U34 methyltransferase, SAM-dependent
C21	snp	1959694	1959694	T	C	argS	NON_SYNONYMOUS_CODING	C/R	COG0018	J	arginyl-tRNA synthetase
C21	snp	1971125	1971125	A	G	cheW	NON_SYNONYMOUS_CODING	V/A	COG0835	NT	purine-binding chemotaxis protein

C21	snp	1972133	1972133	A	G	cheA	NON_SYNONYMOUS_CODING	S/P	COG0643	NT	fused chemotactic sensory histidine kinase in two-component regulatory system with CheB and CheY: sensory histidine kinase/signal sensing protein
C21	indel	2016276	2016277	-	A	fliJ	FRAMESHIFT_CODING	-	COG2882	NUO	flagellar protein
C21	snp	2037966	2037966	G	A	yedY	SYNONYMOUS_CODING	P	COG2041	R	membrane-anchored, periplasmic TMAO, DMSO reductase
C21	snp	2044469	2044469	C	T	yeeJ	NON_SYNONYMOUS_CODING	P/L	-	-	probable adhesin
C21	snp	2081468	2081468	T	C	sbcB	NON_SYNONYMOUS_CODING	V/A	COG2925	L	exonuclease I
C21	snp	2180057	2180057	C	T	yegW	SYNONYMOUS_CODING	*	COG2188	K	predicted DNA-binding transcriptional regulator
C21	snp	2208976	2208976	A	T	yehQ	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	2247576	2247576	T	C	yeiE	NON_SYNONYMOUS_CODING	Q/R	COG0583	K	predicted DNA-binding transcriptional regulator
C21	snp	2277333	2277333	T	C	bcr	SYNONYMOUS_CODING	A	COG2814	G	bicyclomycin/multidrug efflux system
C21	snp	2360599	2360599	T	C	yfaY	NON_SYNONYMOUS_CODING	S/G	COG1058	R	conserved protein
C21	snp	2407281	2407281	T	C	yfbR	NON_SYNONYMOUS_CODING	V/A	COG1896	R	5'-nucleotidase
C21	indel	2483331	2483332	-	C	evgS	FRAMESHIFT_CODING	-	COG0642	T	hybrid sensory histidine kinase in two-component regulatory system with EvgA
C21	snp	2520915	2520915	T	C	xapB	NON_SYNONYMOUS_CODING	S/G	COG2211	G	xanthosine transporter
C21	snp	2554980	2554980	A	G	eutC	NON_SYNONYMOUS_CODING	W/R	COG4302	E	ethanolamine ammonia-lyase, small subunit (light chain)
C21	snp	2556896	2556896	T	C	intZ	NON_SYNONYMOUS_CODING	L/P	COG0582	L	CPZ-55 prophage; predicted integrase
C21	snp	2573112	2573112	G	A	eutP	NON_SYNONYMOUS_CODING	P/L	COG4917	E	conserved protein with nucleoside triphosphate hydrolase domain
C21	snp	2609439	2609439	A	G	hyfI	NON_SYNONYMOUS_CODING	S/G	COG3260	C	hydrogenase 4, Fe-S subunit
C21	snp	2641755	2641755	T	C	rImN	NON_SYNONYMOUS_CODING	N/S	COG0820	R	23S rRNA m(2)A2503 methyltransferase, SAM-dependent
C21	snp	2853870	2853870	G	A	fhIA	NON_SYNONYMOUS_CODING	R/H	COG3604	KT	DNA-binding transcriptional activator

C21	snp	2935824	2935824	A	G	fucK	NON_SYNONYMOUS_CODING	D/G	COG1070	G	L-fuculokinase
C21	snp	3119818	3119818	T	C	glcB	SYNONYMOUS_CODING	Q	COG2225	C	malate synthase G
C21	snp	3122613	3122613	G	A	glcF	NON_SYNONYMOUS_CODING	P/L	COG0247	C	glycolate oxidase iron-sulfur subunit
C21	snp	3154895	3154895	G	A	dkgA	NON_SYNONYMOUS_CODING	R/H	COG0656	R	2,5-diketo-D-gluconate reductase A
C21	snp	3176187	3176187	T	C	tolC	SYNONYMOUS_CODING	S	COG1538	MU	transport channel
C21	snp	3176753	3176753	A	G	tolC	NON_SYNONYMOUS_CODING	Q/R	COG1538	MU	transport channel
C21	snp	3177340	3177340	T	C	tolC	NON_SYNONYMOUS_CODING	Y/H	COG1538	MU	transport channel
C21	snp	3193359	3193359	G	A	hldE	STOP_GAINED	Q/*	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	3194503	3194503	G	A	hldE	SYNONYMOUS_CODING	V	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	3211874	3211874	T	C	rpoD	NON_SYNONYMOUS_CODING	L/P	COG0568	K	RNA polymerase, sigma 70 (sigma D) factor
C21	snp	3233809	3233809	G	A	rImG	NON_SYNONYMOUS_CODING	A/V	COG2813	J	23S rRNA mG1835 methyltransferase, SAM-dependent
C21	snp	3246194	3246194	T	C	yqjA	NON_SYNONYMOUS_CODING	F/L	COG0586	S	required, with yghB, for membrane integrity; inner membrane protein
C21	snp	3322912	3322912	T	C	folP	NON_SYNONYMOUS_CODING	T/A	COG0294	H	7,8-dihydropteroate synthase
C21	snp	3356518	3356518	G	A	gltB	NON_SYNONYMOUS_CODING	D/N	COG0069	E	glutamate synthase, large subunit
C21	snp	3364975	3364975	G	A	yhcF	NON_SYNONYMOUS_CODING	G/R	-	-	predicted transcriptional regulator
C21	snp	3369748	3369748	G	A	nanT	SYNONYMOUS_CODING	V	COG2814	G	sialic acid transporter
C21	snp	3462098	3462098	T	C	gspL	NON_SYNONYMOUS_CODING	V/A	COG3297	U	general secretory pathway component, cryptic
C21	snp	3542361	3542361	G	A	bioH	NON_SYNONYMOUS_CODING	P/L	COG0596	R	carboxylesterase of pimeloyl-CoA synthesis
C21	snp	3753588	3753588	T	C	aldB	NON_SYNONYMOUS_CODING	Q/R	COG1012	C	aldehyde dehydrogenase B
C21	snp	3794765	3794765	A	G	rfaC	NON_SYNONYMOUS_CODING	K/R	COG0859	M	ADP-heptose:LPS heptosyl transferase I
C21	snp	3831732	3831732	A	G	yicI	NON_SYNONYMOUS_CODING	F/L	COG1501	G	predicted alpha-glucosidase
C21	snp	3867170	3867170	G	A	yidR	NON_SYNONYMOUS_CODING	R/C	COG0823	U	conserved protein
C21	snp	3923701	3923701	G	A	mnmG	5PRIME_UTR	-	COG0445	D	5-methylaminomethyl-2-thiouridine modification at tRNA U34

C21	snp	4051916	4051916	C	T	glnG	SYNONYMOUS_CODING	K	COG2204	T	fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator/sigma54 interaction protein
C21	snp	4054114	4054114	C	T	glnL	SYNONYMOUS_CODING	L	COG3852	T	sensory histidine kinase in two-component regulatory system with GlnG
C21	snp	4085593	4085593	A	G	yiiG	NON_SYNONYMOUS_CODING	H/R	-	-	conserved lipoprotein
C21	snp	4111725	4111725	T	C	uspD	NON_SYNONYMOUS_CODING	V/A	COG0589	T	stress-induced protein
C21	indel	4159177	4159178	-	C	fabR	FRAMESHIFT_CODING	-	COG1309	K	DNA-binding transcriptional repressor
C21	snp	4161425	4161425	G	A	btuB	5PRIME_UTR	-	COG4206	H	vitamin B12/cobalamin outer membrane transporter
C21	indel	4271828	4271828	G	-	uvrA	FRAMESHIFT_CODING	-	COG0178	L	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC
C21	snp	4407528	4407528	A	G	rImB	SYNONYMOUS_CODING	G	COG0566	J	23S rRNA (Gm2251)-methyltransferase
C21	indel	4441815	4441815	G	-	ytfM	FRAMESHIFT_CODING	-	COG0729	M	predicted outer membrane protein and surface antigen
C21	indel	4473579	4473580	-	G	yjgL	FRAMESHIFT_CODING	-	-	-	predicted protein
C21	snp	4490470	4490470	C	T	idnT	NON_SYNONYMOUS_CODING	A/T	COG2610	GE	L-idonate and D-gluconate transporter
C21	snp	4517532	4517532	A	G	yjhU	SYNONYMOUS_CODING	I	COG2390	K	KpLE2 phage-like element; predicted DNA-binding transcriptional regulator
C21	snp	4526189	4526189	A	G	sgcQ	NON_SYNONYMOUS_CODING	V/A	COG0434	R	KpLE2 phage-like element; predicted nucleoside triphosphatase
C21	snp	4567683	4567683	C	T	yjiP	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C21	snp	4589938	4589938	G	A	tsr	NON_SYNONYMOUS_CODING	V/I	COG0840	NT	methyl-accepting chemotaxis protein I, serine sensor receptor

C22	snp	21442	21442	G	A	ribF	SYNONYMOUS_CODING	Q	COG0196	H	bifunctional riboflavin kinase/FAD synthetase
C22	snp	48106	48106	A	G	kefC	NON_SYNONYMOUS_CODING	Q/R	COG0475	P	potassium:proton antiporter
C22	snp	64216	64216	C	T	polB	NON_SYNONYMOUS_CODING	R/H	COG0417	L	DNA polymerase II
	snp	76664	76664	C	T	sgrR	SYNONYMOUS_CODING		COG4533	R	transcriptional DNA-binding transcriptional activator of sgrS sRNA
C22	snp	81083	81083	G	A	leuB	SYNONYMOUS_CODING	G	COG0473	CE	3-isopropylmalate dehydrogenase
C22	snp	95687	95687	A	G	murF	SYNONYMOUS_CODING	V	COG0770	M	UDP-N-acetyl muramoyl-tripeptide:D-alanyl-D-alanine ligase
C22	snp	97551	97551	C	T	murD	SYNONYMOUS_CODING	Y	COG0771	M	UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase
C22	snp	114829	114829	A	G	hofC	NON_SYNONYMOUS_CODING	L/P	COG1459	NU	assembly protein in type IV pilin biogenesis, transmembrane protein
C22	snp	178904	178904	A	G	mtnN	SYNONYMOUS_CODING	L	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	329644	329644	A	G	betT	NON_SYNONYMOUS_CODING	T/A	COG1292	M	choline transporter of high affinity
C22	snp	352488	352488	C	T	prpE	NON_SYNONYMOUS_CODING	H/Y	COG0365	I	propionate--CoA ligase
C22	snp	385577	385577	T	C	tauB	SYNONYMOUS_CODING	G	COG4525	P	taurine transporter subunit
C22	indel	389540	389541	-	T	yaiT	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	392842	392842	G	A	yaiT	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	401199	401199	G	A	phoA	NON_SYNONYMOUS_CODING	D/N	COG1785	P	bacterial alkaline phosphatase
C22	snp	495410	495410	T	C	htpG	NON_SYNONYMOUS_CODING	V/A	COG0326	O	molecular chaperone HSP90 family
C22	snp	500572	500572	A	G	gsk	SYNONYMOUS_CODING	V	COG0524	G	inosine/guanosine kinase
C22	snp	510896	510896	T	C	glsA1	NON_SYNONYMOUS_CODING	V/A	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	517157	517157	A	G	ybbN	NON_SYNONYMOUS_CODING	L/P	COG3118	O	DnaK co-chaperone, thioredoxin-like protein
C22	snp	517804	517804	A	G	ybbO	SYNONYMOUS_CODING	G	COG0300	R	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain
C22	snp	524652	524652	A	G	rhsD	NON_SYNONYMOUS_CODING	Q/R	COG3209	M	rhsD element protein
C22	snp	547694	547694	A	G	ylbE	SYNONYMOUS_CODING	E	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	indel	547831	547832	-	G	ylbE	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	549600	549600	A	G	ylbF	NON_SYNONYMOUS_CODING	T/A	-	-	conserved protein

C22	indel	560913	560914	-	G	sfmD	FRAMESHIFT_CODING	-	COG3188	NU	predicted outer membrane export usher protein
C22	snp	609015	609015	T	C	entD	SYNONYMOUS_CODING	L	COG2977	Q	phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex
C22	snp	626595	626595	A	G	entE	NON_SYNONYMOUS_CODING	I/V	COG1021	Q	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex
C22	snp	686392	686392	G	A	gltI	SYNONYMOUS_CODING	T	COG0834	ET	glutamate and aspartate transporter subunit
C22	indel	867638	867638	C	-	gsiA	FRAMESHIFT_CODING	-	COG1123	R	glutathione transporter ATP-binding protein, ABC superfamily
C22	snp	877125	877125	G	T	rimO	NON_SYNONYMOUS_CODING	A/E	COG0621	J	ribosomal protein S12 methylthiotransferase; radical SAM superfamily
C22	snp	894684	894684	T	C	potG	SYNONYMOUS_CODING	R	COG3842	E	putrescine transporter subunit: ATP-binding component of ABC superfamily
C22	indel	913399	913400	-	A	ybjE	FRAMESHIFT_CODING	-	COG2431	S	predicted transporter
C22	snp	921252	921252	A	G	macB	SYNONYMOUS_CODING	V	COG1136	V	fused macrolide transporter subunits of ABC superfamily: ATP-binding component/membrane component
C22	snp	966954	966954	A	G	msbA	NON_SYNONYMOUS_CODING	T/A	COG1132	V	fused lipid transporter subunits of ABC superfamily: membrane component/ATP-binding component
C22	snp	1015393	1015393	C	T	fabA	NON_SYNONYMOUS_CODING	E/K	COG0764	I	beta-hydroxydecanoyl thioester dehydrase
C22	indel	1026029	1026030	-	C	mgsA	FRAMESHIFT_CODING	-	COG1803	G	methylglyoxal synthase
C22	snp	1059816	1059816	C	T	torA	SYNONYMOUS_CODING	S	COG0243	C	trimethylamine N-oxide (TMAO) reductase I, catalytic subunit
C22	snp	1093365	1093365	C	T	ycdT	STOP_GAINED	R/*	COG3706	T	diguanylate cyclase

C22	snp	1194738	1194738	A	G	icd	SYNONYMOUS_CODING	V	COG0538	C	e14 prophage; isocitrate dehydrogenase, specific for NADP+
C22	indel	1293726	1293726	G	-	insZ	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	1298991	1298991	G	A	oppB	5PRIME_UTR	-	COG0601	EP	oligopeptide transporter subunit
C22	snp	1356669	1356669	T	C	puuP	SYNONYMOUS_CODING	G	COG0531	E	putrescine importer
C22	indel	1377889	1377890	-	G	ycjT	FRAMESHIFT_CODING	-	COG1554	G	predicted hydrolase
C22	indel	1435247	1435247	T	-	MicC	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	1456641	1456641	A	G	paaG	SYNONYMOUS_CODING	A	COG1024	I	predicted enoyl-CoA hydratase
C22	snp	1549184	1549184	C	T	fdnH	NON_SYNONYMOUS_CODING	P/S	COG0437	C	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible
C22	indel	1592272	1592273	-	C	yneO	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	1645619	1645619	G	A	ydfX	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	1731204	1731204	G	A	lhr	NON_SYNONYMOUS_CODING	G/D	COG1201	R	predicted ATP-dependent helicase
C22	snp	1873938	1873938	G	A	yeaN	NON_SYNONYMOUS_CODING	S/N	COG2807	P	predicted transporter
C22	snp	1913971	1913971	T	C	yebR	NON_SYNONYMOUS_CODING	Q/R	COG1956	T	free methionine-(R)-sulfoxide reductase
C22	snp	1951551	1951551	A	G	cmoB	NON_SYNONYMOUS_CODING	N/S	COG2227	H	tRNA mo(5)U34 methyltransferase, SAM-dependent
C22	snp	1964524	1964524	G	A	cheZ	NON_SYNONYMOUS_CODING	R/C	COG3143	NT	chemotaxis regulator, protein phosphatase for CheY
C22	snp	2007291	2007291	G	A	yedE	NON_SYNONYMOUS_CODING	V/M	COG2391	R	predicted inner membrane protein
C22	snp	2014597	2014597	G	A	fliI	NON_SYNONYMOUS_CODING	R/H	COG1157	NU	flagellum-specific ATP synthase
C22	snp	2034663	2034663	T	C	hchA	SYNONYMOUS_CODING	L	COG0693	R	Hsp31 molecular chaperone
C22	snp	2272188	2272188	A	G	yejA	SYNONYMOUS_CODING	K	COG4166	E	microcin C transporter YejABEF, periplasmic binding protein; ABC family
C22	snp	2356185	2356185	G	A	yfaU	NON_SYNONYMOUS_CODING	A/V	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	2414786	2414786	T	C	pta	NON_SYNONYMOUS_CODING	L/P	COG0857	R	phosphate acetyltransferase

C22	snp	2492972	2492972	T	C	ypdI	NON_SYNONYMOUS_CODING	Y/H	-	-	predicted lipoprotein involved in colanic acid biosynthesis
C22	snp	2532053	2532053	T	C	ptsI	5PRIME_UTR	-	COG1080	G	PEP-protein phosphotransferase of PTS system (enzyme I)
C22	snp	2593249	2593249	T	C	ypfI	SYNONYMOUS_CODING	Q	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	2682993	2682993	G	A	glyA	SYNONYMOUS_CODING	G	COG0112	E	serine hydroxymethyltransferase
C22	snp	2683583	2683583	T	C	glyA	5PRIME_UTR	-	COG0112	E	serine hydroxymethyltransferase
C22	snp	2794168	2794168	C	T	ygaE	NON_SYNONYMOUS_CODING	A/V	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	2794938	2794938	T	C	yqaE	NON_SYNONYMOUS_CODING	Y/C	COG0401	S	regulated by cyaR sRNA, UPF0057 family; predicted membrane protein
C22	indel	2822518	2822518	G	-	mltB	FRAMESHIFT_CODING	-	COG2951	M	membrane-bound lytic murein transglycosylase B
C22	snp	2846778	2846778	A	G	hycC	SYNONYMOUS_CODING	T	COG0651	CP	hydrogenase 3, membrane subunit
C22	snp	2892481	2892481	T	C	ygcP	SYNONYMOUS_CODING	S	COG1954	K	predicted anti-terminator regulatory protein
C22	snp	2924262	2924262	G	A	ygdH	UPSTREAM (-68)	-	COG1611	R	conserved protein, UPF0717 family
C22	snp	2930004	2930004	T	C	fucO	SYNONYMOUS_CODING	V	COG1454	C	L-1,2-propanediol oxidoreductase
C22	snp	2935824	2935824	A	G	fucK	NON_SYNONYMOUS_CODING	D/G	COG1070	G	L-fuculokinase
C22	snp	2978919	2978919	C	T	araE	STOP_GAINED	W/*	COG2814	G	arabinose transporter
C22	snp	2991561	2991561	A	G	ygeI	UPSTREAM (-99)	-	-	-	predicted protein
C22	snp	3048078	3048078	C	T	gcvT	SYNONYMOUS_CODING	A	COG0404	E	aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex
C22	indel	3100356	3100357	-	C	trmB	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	3126227	3126227	A	G	glcC	UPSTREAM (-1)	-	COG2186	K	DNA-binding transcriptional dual regulator, glycolate-binding
C22	snp	3145438	3145438	T	C	yghX	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND

C22	snp	3168182	3168182	G	A	qseB	SYNONYMOUS_CODING	R	COG0745	TK	quorum sensing DNA-binding response regulator in two-component regulatory system with QseC
C22	snp	3176270	3176270	A	G	tolC	NON_SYNONYMOUS_CODING	D/G	COG1538	MU	transport channel
C22	snp	3176601	3176601	C	T	tolC	SYNONYMOUS_CODING	I	COG1538	MU	transport channel
C22	snp	3176753	3176753	A	G	tolC	NON_SYNONYMOUS_CODING	Q/R	COG1538	MU	transport channel
C22	snp	3176813	3176813	A	G	tolC	NON_SYNONYMOUS_CODING	D/G	COG1538	MU	transport channel
C22	snp	3177340	3177340	T	C	tolC	NON_SYNONYMOUS_CODING	Y/H	COG1538	MU	transport channel
C22	snp	3177366	3177366	T	C	tolC	SYNONYMOUS_CODING	N	COG1538	MU	transport channel
C22	snp	3206772	3206772	A	G	ttdT	NON_SYNONYMOUS_CODING	S/G	COG0471	P	L-tartrate/succinate antiporter
C22	snp	3233951	3233951	T	C	ygjP	UPSTREAM (-31)	-	COG1451	R	predicted metal dependent hydrolase
C22	snp	3244782	3244782	T	C	exuR	NON_SYNONYMOUS_CODING	F/L	COG2186	K	DNA-binding transcriptional repressor
C22	indel	3268503	3268504	-	C	RNaseP_bact_a	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	3339659	3339659	A	G	kdsD	SYNONYMOUS_CODING	V	COG0794	M	D-arabinose 5-phosphate isomerase
C22	snp	3364975	3364975	G	A	yhcF	NON_SYNONYMOUS_CODING	G/R	-	-	predicted transcriptional regulator
C22	snp	3476899	3476899	G	A	kefB	SYNONYMOUS_CODING	R	COG0475	P	potassium:proton antiporter
C22	snp	3533758	3533758	G	A	envZ	STOP_GAINED	Q/*	COG0642	T	sensory histidine kinase in two-component regulatory system with OmpR
C22	snp	3555218	3555218	T	C	rtcB	NON_SYNONYMOUS_CODING	Y/C	COG1690	S	conserved protein
C22	snp	3830564	3830564	T	C	yicI	NON_SYNONYMOUS_CODING	N/S	COG1501	G	predicted alpha-glucosidase
C22	snp	3880833	3880833	A	G	dnaA	NON_SYNONYMOUS_CODING	M/T	COG0593	L	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator
C22	snp	3908724	3908724	C	T	pstS	STOP_GAINED	W/*	COG0226	P	periplasmic phosphate binding protein, high-affinity

C22	snp	3947340	3947340	G	A	yifB	NON_SYNONYMOUS_CODING	P/L	COG0606	O	predicted bifunctional enzyme and transcriptional regulator
C22	indel	3968441	3968443	ACG	-	wecB	NON_SYNONYMOUS_CODING	T/-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	snp	3978613	3978613	C	T	wecG	NON_SYNONYMOUS_CODING	T/M	NOT_FOUND	NOT_FOUND	NOT_FOUND
C22	indel	4122303	4122303	C	-	cytR	FRAMESHIFT_CODING	-	COG1609	K	DNA-binding transcriptional dual regulator
C22	indel	4159177	4159178	-	C	fabR	FRAMESHIFT_CODING	-	COG1309	K	DNA-binding transcriptional repressor
C22	snp	4222412	4222412	A	G	metH	NON_SYNONYMOUS_CODING	N/D	COG1410	E	homocysteine-N5-methyltetrahydrofolate transmethylase, B12-dependent
C22	indel	4364734	4364735	-	C	dcuA	FRAMESHIFT_CODING	-	COG2704	R	C4-dicarboxylate antiporter
C22	snp	4370483	4370483	A	G	groL	NON_SYNONYMOUS_CODING	N/S	COG0459	O	Cpn60 chaperonin GroEL, large subunit of GroESL
C22	snp	4420466	4420466	A	G	ulaD	SYNONYMOUS_CODING	V	COG0269	G	3-keto-L-gulonate 6-phosphate decarboxylase
C22	snp	4432875	4432875	C	T	cpdB	NON_SYNONYMOUS_CODING	A/T	COG0737	F	2':3'-cyclic-nucleotide 2'-phosphodiesterase
C22	snp	4510965	4510965	A	G	fecC	SYNONYMOUS_CODING	G	COG0609	P	KpLE2 phage-like element; iron-dicitrate transporter subunit
C22	snp	4576825	4576825	A	G	mcrB	NON_SYNONYMOUS_CODING	I/T	COG1401	V	5-methylcytosine-specific restriction enzyme McrBC, subunit McrB
C23	snp	31174	31174	G	A	carB	NON_SYNONYMOUS_CODING	A/T	COG0458	EF	carbamoyl-phosphate synthase large subunit
C23	snp	86391	86391	A	G	ilvI	SYNONYMOUS_CODING	A	COG0028	EH	acetolactate synthase III, large subunit
C23	snp	109201	109201	A	G	secA	NON_SYNONYMOUS_CODING	H/R	COG0653	U	preprotein translocase subunit, ATPase
C23	snp	155935	155935	T	C	ecpD	SYNONYMOUS_CODING	K	COG3121	NU	predicted periplasmic pilin chaperone
C23	snp	255356	255356	C	T	pepD	NON_SYNONYMOUS_CODING	A/T	COG2195	E	aminoacyl-histidine dipeptidase (peptidase D)
C23	snp	348383	348383	G	A	prpB	NON_SYNONYMOUS_CODING	D/N	COG2513	G	2-methylisocitrate lyase
C23	snp	402393	402393	G	T	psiF	5PRIME_UTR	-	-	-	conserved protein, PsiF family, pho regulon
C23	indel	410116	410117	-	G	mak	FRAMESHIFT_CODING	-	COG1940	KG	manno(fructo)kinase

C23	snp	544887	544887	A	G	alID	NON_SYNONYMOUS_CODING	V/A	COG2055	C	ureidoglycolate dehydrogenase
C23	snp	547694	547694	A	G	ylbE	SYNONYMOUS_CODING	E	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	indel	547831	547832	-	G	ylbE	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	701381	701381	C	T	nagA	SYNONYMOUS_CODING	A	COG1820	G	N-acetylglucosamine-6-phosphate deacetylase
C23	snp	839948	839948	G	A	fiu	SYNONYMOUS_CODING	I	COG4774	P	catecholate siderophore receptor Fiu
C23	snp	856139	856139	C	T	ybiT	SYNONYMOUS_CODING	N	COG0488	R	fused predicted transporter subunits of ABC superfamily: ATP-binding components
C23	snp	878192	878192	C	T	yliI	SYNONYMOUS_CODING	D	COG2133	G	soluble aldose sugar dehydrogenase
C23	snp	900391	900391	G	A	artM	STOP_GAINED	Q/*	COG4160	E	arginine transporter subunit
C23	snp	940791	940791	T	C	dmsA	NON_SYNONYMOUS_CODING	Y/H	COG0243	C	dimethyl sulfoxide reductase, anaerobic, subunit A
C23	snp	940992	940992	G	A	dmsA	NON_SYNONYMOUS_CODING	D/N	COG0243	C	dimethyl sulfoxide reductase, anaerobic, subunit A
C23	snp	971270	971270	C	T	ycbJ	NON_SYNONYMOUS_CODING	S/L	-	-	conserved protein
C23	snp	1028847	1028847	T	C	rImI	NON_SYNONYMOUS_CODING	T/A	COG1092	R	23S rRNA m(5)C1962 methyltransferase, SAM-dependent
C23	indel	1083798	1083799	-	G	ycdB	FRAMESHIFT_CODING	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	indel	1094834	1094835	-	A	ymdE	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	1134404	1134404	C	T	flgG	SYNONYMOUS_CODING	I	COG4786	N	flagellar component of cell-distal portion of basal-body rod
C23	snp	1214078	1214078	C	T	ycgF	SYNONYMOUS_CODING	G	COG2200	T	anti-repressor for YcgE, blue light-responsive; FAD-binding; has c-di-GMP phosphodiesterase-like EAL domain, but does not degrade c-di-GMP
C23	indel	1418811	1418812	-	G	ydaT	FRAMESHIFT_CODING	-	-	-	Rac prophage; predicted protein

C23	snp	1438612	1438612	G	A	ydbK	NON_SYNONYMOUS_CODING	T/I	COG0674	C	fused predicted pyruvate-flavodoxin oxidoreductase: conserved protein/conserved protein/FeS binding protein
C23	snp	1456641	1456641	A	G	paaG	SYNONYMOUS_CODING	A	COG1024	I	predicted enoyl-CoA hydratase
C23	snp	1470771	1470771	C	T	ydbA	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	1478597	1478597	C	T	ynbC	NON_SYNONYMOUS_CODING	P/L	COG2267	I	predicted hydrolase
C23	indel	1506241	1506241	G	-	ydcP	FRAMESHIFT_CODING	-	COG0826	O	predicted peptidase
C23	indel	1590763	1590764	-	C	yneO	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	1605564	1605564	G	A	tam	SYNONYMOUS_CODING	P	COG4106	R	trans-aconitate methyltransferase
C23	snp	1858728	1858728	T	C	ydjL	NON_SYNONYMOUS_CODING	D/G	COG1063	ER	predicted oxidoreductase, Zn-dependent and NAD(P)-binding
C23	indel	1887631	1887632	-	C	fadD	FRAMESHIFT_CODING	-	COG0318	IQ	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)
C23	snp	1934359	1934359	T	C	zwf	5PRIME_UTR	-	COG0364	G	glucose-6-phosphate 1-dehydrogenase
C23	snp	1934660	1934660	T	C	hexR	UPSTREAM (-16)	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	1946339	1946339	C	T	nudB	SYNONYMOUS_CODING	A	COG0494	LR	dihydronopterin triphosphate pyrophosphatase
C23	snp	1964142	1964142	T	C	flhB	NON_SYNONYMOUS_CODING	Q/R	COG1377	NU	flagellin export apparatus, substrate specificity protein
C23	snp	2031261	2031261	G	A	yedR	NON_SYNONYMOUS_CODING	A/V	-	-	inner membrane protein
C23	snp	2041770	2041770	G	A	mtfA	SYNONYMOUS_CODING	T	COG3228	S	anti-repressor for DgsA(Mlc)
C23	snp	2120281	2120281	G	A	manB	SYNONYMOUS_CODING	G	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	2125083	2125083	G	A	fcl	SYNONYMOUS_CODING	S	COG0451	MG	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase/ GDP-4-dehydro-6-L-deoxygalactose reductase
C23	snp	2157936	2157936	A	G	mdtC	SYNONYMOUS_CODING	V	COG0841	V	multidrug efflux system, subunit C

C23	snp	2235267	2235267	G	A	mgIC	NON_SYNONYMOUS_CODING	T/I	COG4211	G	methyl-galactoside transporter subunit
C23	snp	2277333	2277333	T	C	bcr	SYNONYMOUS_CODING	A	COG2814	G	bicyclomycin/multidrug efflux system
C23	snp	2334052	2334052	G	A	yfaA	SYNONYMOUS_CODING	D	COG4685	S	conserved protein, DUF2138 family
C23	snp	2354609	2354609	A	G	glpC	NON_SYNONYMOUS_CODING	Q/R	COG0247	C	sn-glycerol-3-phosphate dehydrogenase (anaerobic), small subunit
C23	snp	2412038	2412038	G	A	ackA	NON_SYNONYMOUS_CODING	G/S	COG0282	C	acetate kinase A and propionate kinase 2
C23	snp	2475477	2475477	T	C	dsdC	NON_SYNONYMOUS_CODING	I/V	COG0583	K	DNA-binding transcriptional dual regulator
C23	snp	2480643	2480643	A	G	emrK	NON_SYNONYMOUS_CODING	V/A	COG1566	V	EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein component
C23	snp	2578169	2578169	C	T	tktB	NON_SYNONYMOUS_CODING	T/M	COG0021	G	transketolase 2, thiamin-binding
C23	snp	2603047	2603047	T	C	hyfD	NON_SYNONYMOUS_CODING	L/P	COG1009	CP	hydrogenase 4, membrane subunit
C23	snp	2614239	2614239	A	G	yfgC	NON_SYNONYMOUS_CODING	S/G	COG4783	R	predicted peptidase, has TPR repeats
C23	indel	2651708	2651709	-	C	IS128	WITHIN_NON_CODING_GENE	-	NOT_FOUND	NOT_FOUND	NOT_FOUND
C23	snp	2708059	2708059	A	G	rpoE	5PRIME_UTR	-	COG1595	K	RNA polymerase, sigma 24 (sigma E) factor
C23	snp	2717738	2717738	G	A	yfiP	NON_SYNONYMOUS_CODING	R/Q	COG3148	S	conserved protein, DTW domain
C23	snp	2776890	2776890	T	C	ypjA	NON_SYNONYMOUS_CODING	T/A	COG3468	MU	adhesin-like autotransporter
C23	indel	2891983	2891985	CAC	-	ygcO	NON_SYNONYMOUS_CODING	H/-	COG2440	C	predicted 4Fe-4S cluster-containing protein
C23	snp	2934953	2934953	T	C	fucI	NON_SYNONYMOUS_CODING	F/L	COG2407	G	L-fucose isomerase
C23	snp	2935824	2935824	A	G	fucK	NON_SYNONYMOUS_CODING	D/G	COG1070	G	L-fuculokinase
C23	snp	3080060	3080060	T	C	yggG	SYNONYMOUS_CODING	D	COG0501	O	heat shock protein binding to Era protein; predicted peptidase
C23	indel	3132833	3132833	T	-	yghT	FRAMESHIFT_CODING	-	COG0125	F	predicted ATP-binding protein
C23	snp	3176187	3176187	T	C	tolC	SYNONYMOUS_CODING	S	COG1538	MU	transport channel
C23	snp	3176541	3176541	T	C	tolC	SYNONYMOUS_CODING	Y	COG1538	MU	transport channel

C23	snp	3176564	3176564	A	G	tolC	NON_SYNONYMOUS_CODING	D/G	COG1538	MU	transport channel
C23	snp	3176582	3176582	A	G	tolC	NON_SYNONYMOUS_CODING	Q/R	COG1538	MU	transport channel
C23	snp	3176753	3176753	A	G	tolC	NON_SYNONYMOUS_CODING	Q/R	COG1538	MU	transport channel
C23	snp	3177340	3177340	T	C	tolC	NON_SYNONYMOUS_CODING	Y/H	COG1538	MU	transport channel
C23	snp	3212411	3212411	G	A	rpoD	NON_SYNONYMOUS_CODING	R/H	COG0568	K	RNA polymerase, sigma 70 (sigma D) factor
C23	snp	3218212	3218212	G	A	patA	NON_SYNONYMOUS_CODING	A/T	COG4992	E	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent
C23	snp	3306890	3306890	G	A	nlpI	SYNONYMOUS_CODING	C	COG4785	R	lipoprotein involved in osmotic sensitivity and filamentation
C23	indel	3328375	3328376	-	T	dacB	FRAMESHIFT_CODING	-	COG2027	M	D-alanyl-D-alanine carboxypeptidase
C23	snp	3357140	3357140	G	A	gltB	NON_SYNONYMOUS_CODING	S/N	COG0069	E	glutamate synthase, large subunit
C23	snp	3364975	3364975	G	A	yhcF	NON_SYNONYMOUS_CODING	G/R	-	-	predicted transcriptional regulator
C23	snp	3389175	3389175	T	C	tldD	SYNONYMOUS_CODING	E	COG0312	R	predicted peptidase
C23	snp	3530385	3530385	T	C	yhgE	NON_SYNONYMOUS_CODING	Y/C	-	-	predicted inner membrane protein
C23	indel	3533587	3533587	C	-	envZ	FRAMESHIFT_CODING	-	COG0642	T	sensory histidine kinase in two-component regulatory system with OmpR
C23	snp	3560885	3560885	A	G	glpD	NON_SYNONYMOUS_CODING	I/V	COG0578	C	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-binding
C23	snp	3896903	3896903	G	A	yieK	NON_SYNONYMOUS_CODING	P/S	COG0363	G	predicted 6-phosphogluconolactonase
C23	snp	4019567	4019567	A	G	ubiB	NON_SYNONYMOUS_CODING	Q/R	COG0661	R	2-octaprenylphenol hydroxylase
C23	indel	4159177	4159178	-	C	fabR	FRAMESHIFT_CODING	-	COG1309	K	DNA-binding transcriptional repressor
C23	snp	4200557	4200557	T	C	zraS	SYNONYMOUS_CODING	I	COG0642	T	sensory histidine kinase in two-component regulatory system with ZraR

C23	snp	4245058	4245058	C	A	malK	STOP_GAINED	Y/*	COG3839	G	fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein
C23	snp	4366062	4366062	C	T	aspA	NON_SYNONYMOUS_CODING	V/I	COG1027	E	aspartate ammonia-lyase
C23	snp	4509897	4509897	T	C	fecD	NON_SYNONYMOUS_CODING	S/G	COG0609	P	KpLE2 phage-like element; iron-dicitrate transporter subunit

Table S9. Total number and type of SNPs observed across the three genomes

SNP: Ref/Var	Fraction of SNPs	Total SNPs	C21	C22	C23	STOP_CODONS
A/G	30.1%	75	26	33	16	0
G/A	25.7%	64	23	20	21	4
C/T	16.5%	41	14	15	12	3
T/C	26.1%	65	22	23	20	0
A/T	0.4%	1	1	0	0	0
G/T	0.8%	2	0	1	1	0
C/A	0.4%	1	0	0	1	1
TRANSITIONS	98.4%	245	85	91	69	7
TRANSVERSIONS	1.6%	4	1	1	2	1

Table S10. Calculation of secondary mutation rates of recoded genomes based on results from Illumina sequencing of three genomes. Three genomes - C21, C22, C23 - have been subjected to ~25-30 rounds of MAGE cycling, dsDNA recombinations to place selectable markers in targeted positions across the genome and two conjugation protocols.

Metric	Average	Total	C21	C22	C23
Secondary mutation rate (INDELS + SNPs + unanno SNPs)	2.52E-08	2.52E-08	2.48E-08	2.86E-08	2.23E-08
Secondary mutation rate (INDELs + SNPs)	2.17E-08	2.17E-08	2.19E-08	2.43E-08	1.90E-08
SNP mutation rate	1.85E-08	1.85E-08	1.92E-08	2.05E-08	1.58E-08
INDEL mutation rate	3.20E-09	3.20E-09	2.68E-09	3.79E-09	3.12E-09
Size of E. coli genome (bp)	4.65E+06	1.39E+07	4.65E+06	4.65E+06	4.65E+06
All Mutations per population per division (INDELS + SNPs + unanno SNPs)	0.12	0.352	0.115	0.133	0.104
Mutations per population per division (INDELs + SNPs)	0.10	0.303	0.102	0.113	0.088
SNPs per population per division	0.09	0.258	0.089	0.095	0.074
INDELS per population per division	0.01	0.045	0.012	0.018	0.015
Calculated No. of cell divisions	964.0	964	964	964	964
Total Mutations (INDELs, SNPs + unanno SNPs) per genome	113.0	339	111	128	100
Total Mutations (INDELs + SNPs) per genome	97.3	292	98	109	85
SNPs per genome	83.0	249	86	92	71
INDELS per genome	14.3	43	12	17	14
Unannotated	15.7	47	13	19	15

Table S11. Estimates for total number of cell divisions: ~25-30 rounds of MAGE cycling, dsDNA recombinations to place selectable markers in targeted positions across the genome and two conjugation protocols.

	Calculated # cell divisions	MAGE		
		divisions per Step	No.	# cell divisions
Total	964	MAGE cycles	6	25
MAGE	366	o/n growths	15	6
Recombinations	258	Re-dilution	5	6
Conjugation 1	127	Colony/Plating	30	2
Intermediate recombination	86	Outgrowth	12	3
Conjugation 2	127	MAGE total		366
Selectable marker dsDNA recombinations				
Step	Divsions per X	Conjugations		
Colony/plating	30	Colony/plating	30	
Outgrowth, mid-log	10	Outgrowth, log-stationary	12	
Induce @ 42C, 15 min	0	Conjugate (2-15 hrs)	10	
Electroporation	0	Positive Selection	15	
Recover 1 hour	0	Dilute 1/100, outgrowth mid-log	6	
Plate o/n	30	Dilute 1/100 in ColE1	6	
Colony outgrowth to mid-log	10	Colony/plating	30	
Dilute, re-grow, freeze	6	Outgrowth, log-stationary	12	
Divisions/recombination	86	Dilute, re-grow, freeze	6	
No. of recombinations	3	Total		127
Total	258			

Table S12. Sequences of MASC-PCR primers

Gene	MASC-PCR_forward_TAG_primer	MASC-PCR_forward_TAA_primer	MASC-PCR_reverse_primer
rbsB	ATCTGAAACTGGTTGTTAACAGCTAG	ATCTGAAACTGGTTGTTAACAGCTAA	CACGCTAGCCCATACACCA
rbsR	GAACCGGGTTCGGCTTAG	GAACCGGGTTCGGCTTAA	TTACTGCTTCTCTATATTCTCCATGCA
ilvL	ACTTGGACGAGGAAAGGCTTAG	ACTTGGACGAGGAAAGGCTTAA	AGCAGGCAACGTCGAATG
ilvA	AGGTTCTTTGGCGGGTTAG	AGGTTCTTTGGCGGGTTAA	TGGCGTTTCGATGCTGG
wzzE	CCGCCGTTGCTCGAAATAG	CCGCCGTTGCTCGAAATAA	TGATAAAACGCCGCCAGG
asIB	CATTGCTGGTGGTGAGTAAGTAG	CATTGCTGGTGGTGAGTAAGTAA	AAGCGACTCCATCGGCG
hemY	CAGAATAACCCGCCACAGTAG	CAGAATAACCCGCCACAGTAA	TTCCGCCTAGTGCCTCATAAAC
yigG	TGCACCTACTGATTCATAAAACAATAG	TGCACCTACTGATTCATAAAACAATAA	TTGAATAGTTAACCGTTGTCTACTTTAATG
recQ	TGATGGCGATGACGAAGAGTAG	TGATGGCGATGACGAAGAGTAA	TCGGGACCGGGGCT
rmuC	GAATATAATCAGCAGTCGCGCTAG	GAATATAATCAGCAGTCGCGCTAA	AAAAATTGTTCCAGAAGTGTAAACAGATTG
tatD	CACTGTTGGGATTGCGTTTAG	CACTGTTGGGATTGCGTTTAA	GAGTAGCCTTAGGTTTCGAAC
yihL	CCGTAGACCTCATCATTAACTGTAG	CCGTAGACCTCATCATTAACTGTAA	TACAGGCTTTATGACCCAGGC
yihW	CCCCAGGAAGACCGCTAG	CCCCAGGAAGACCGCTAA	CCGTATCGCTGGGTAAAAAC
yiiD	GGGGGAACGAAGAAGAGTAG	GGGGGAACGAAGAAGAGTAA	GGGAAAGTTGTTTCTAAATTAAACACAGA
cpxP	TAGCAACTCACGTTCCCAGTAG	TAGCAACTCACGTTCCCAGTAA	TTACCGTGACCAAACGAGTGA
frwD	GCAAACCCATCTTATTCTGGAGTAG	GCAAACCCATCTTATTCTGGAGTAA	CGAATCTGTTGCACAGGCG
zraR	TGGCAAAACTGTCGCGTTAG	TGGCAAAACTGTCGCGTTAA	GGCCTGCCGCTGGA
yjAB	GCGTATGTGGGGCGTAG	GCGTATGTGGGGCGTAA	CGCATTCTCCATGAAGTGGTC
yjdK	ATGACTATTCGTCAGTTTACAAGTAG	ATGACTATTCGTCAGTTTACAAGTAA	TATGTGTTTCTCATGTGAGATAAACCAAG
blc	GGTACAGCAGCCTGGTAGTTAG	GGTACAGCAGCCTGGTAGTTAA	TGAGTCGCTAACCGATG
ulaF	CGCTTATTACGGGCAGAAGTAG	CGCTTATTACGGGCAGAAGTAA	CTGCACCAGTGATGGCAG
yjFY	CAGCGCGGATATTATCGCTAG	CAGCGCGGATATTATCGCTAA	TACGAAACCATGAAAGCGGC
priB	CAGATTGAATTGATAGATTCTGGAGACTAG	CAGATTGAATTGATAGATTCTGGAGACTAA	GATGTCGCGAGTACCGATG
ytfB	AGTTTATTGTCGCGCGTAG	AGTTTATTGTCGCGCGTAA	CTTCCACGCCCTACACCGTA
ytfG	GCGTAAGCCATCTTTAATGTTAATAACTAG	GCGTAAGCCATCTTTAATGTTAATAACTAA	TTGAATGGCACTGGCAAGG
msrA	GCCGCCGGAAAGCATAG	GCCGCCGGAAAGCATAA	AAGTTGATTAATTGTGTGAAATACACATTGA
ytfN	GGATTGCTCTATCAGTCGAGTTTAG	GGATTGCTCTATCAGTCGAGTTTAA	CGCCCCCTGGTGC
b4250	TCGTGATGATCGCCGGTAG	TCGTGATGATCGCCGGTAA	GATGCCGCCCTGGCG
idnR	ATCACGGCAACACGCTTAA	ATCACGGCAACACGCTTAA	AGTAAAAACAGTTCTGTGTCGG
b4273	GGTTAAGTGATAACAGATGTCGAAATATAA	GGTTAAGTGATAACAGATGTCGAAATATAA	GTCGCTGTACTGAAAAGTATTCTGTA
yjgX	CGTGTGACAGCCTTAACCTCTAG	CGTGTGACAGCCTTAACCTCTAA	ACACGCCAGTCGCC

b4283	TGGAGAATGAAATATTAAAAAGGCTACTGTAG	TGGAGAATGAAATATTAAAAAGGCTACTGTAA	CGAATATCACCTGAGACAATTATAAAAACG
fecE	CCGATGTGCCATTAGAGGTAG	CCGATGTGCCATTAGAGGTAA	GATCCATCAACTGGCCTGTATAAC
nanC	GCATTGGTGTGTCATTAACTGTAG	GCATTGGTGTGTCATTAACTGTAA	TTGAAGATATTCTGGTTAACACCACC
fimB	ACAGCGTCACGCTTTTAG	ACAGCGTCACGCTTTTATAA	GAGTGATGTGGCTACAGTCATTAC
yjN	GTTCCCCCTCGCAATTAGG	GTTCCCCCTCGCAATTAGG	CAACCGCACGGCTG
yjiP	CTATTCCATGGCGGTGATGTAG	CTATTCCATGGCGGTGATGTAA	GATCAACTCCAACAGGGCG
mcrB	GACCAACAAATTATTAGGGGACTCATAG	GACCAACAAATTATTAGGGGACTCATAA	AGCCCTCGCGTGAAG
yjjQ	ATTAAGAAGAGAAATGTCGCACTCATAG	ATTAAGAAGAGAAATGTCGCACTCATAA	CGAGATCCGCGACATGG
yjjV	ATACGTTGTTAACGTGCCGTAG	ATACGTTGTTAACGTGCCGTAA	GCATGATAAGACGCGTTAAGCG
lpIA	GCGGGGGCTGTAAGGTAG	GCGGGGGCTGTAAGGTAA	GATTACTGCACAAACACCCCTGC
creC	GACTTCACCGTCACTCACATAG	GACTTCACCGTCACTCACATAA	CCGGTACCGCTTAAATTCAAGG
kefF	CAGGAGGCCCATCATGGATAG	CAGGAGGCCCATCATGGATAA	ACCACCAAGCACCGAGCG
yabl	GCGTAAAGTGGTGGGTTAG	GCGTAAAGTGGTGGGTTAA	CTATCGCCGCCAGATGG
thiQ	CACTATTGGGGATTACGGGTTAG	CACTATTGGGGATTACGGGTTAA	ATT CCTGCCGGAATGCAGA
murF	CTTTACAGGAGAATGGGACATGTAG	CTTTACAGGAGAATGGGACATGTAA	GACGGGTAAGCCCACAGC
mutT	TTGCGAAGCTAACGTCTGTAG	TTGCGAAGCTAACGTCTGTAA	CCAAAGCAGTGACATTGTCTGA
pdhR	CGTCTGGAGCAACGAAAGAATTAG	CGTCTGGAGCAACGAAAGAATTAA	GGAAACGTTCTGACATGGTTATT
sfsA	AAATCACTGCCGGTTACATTGTAG	AAATCACTGCCGGTTACATTGTAA	AGGCCGCTATAATAGCAGATG
btuF	AATGCGCTTCACAGGTAGATTAG	AATGCGCTTCACAGGTAGATTAA	TACCGCTGTGCCGACTATATC
cdaR	TACAACGGATGAAGAGCGGTAG	TACAACGGATGAAGAGCGGTAA	GCCATACTCACGGCGG
yael	ACGATGCTGGAACGGGTAG	ACGATGCTGGAACGGGTAG	GTTGCTGCTGTATGTGGCG
yafL	TTTGACGGAAGAGACGATTTGTAG	TTTGACGGAAGAGACGATTTGTAA	ATGGCCAATCACTCACTTG
yagY	GGTGATAAGTTCATTCCCGTGAATAG	GGTGATAAGTTCATTCCCGTGAATAA	GCGCTTCGCGCTTGA
eaeh	AGTGCCTCTTACCCAGCAATAG	AGTGCCTCTTACCCAGCAATAA	CTCAGCCTGATGTTTCAATAAGAC
b0299	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTA	TATTTTGCGCAACTCATTTAAATATGACATTGA
yahL	ACGTTAAAATCCGCTACACTCTTAG	ACGTTAAAATCCGCTACACTCTTAA	AACACATTCACAAACATCTGCATG
yahM	CGGCAAATCAGGTTGATTACGTAG	CGGCAAATCAGGTTGATTACGTAA	CGCATCAATTATCTGGCGAGTT
prpE	GCCAGCGATGGAAGAGTAG	GCCAGCGATGGAAGAGTAA	GTGTCGGATGCGACGC
cynR	GGCGGAAATGAATCACGGTAG	GGCGGAAATGAATCACGGTAA	GCCTACGTAGAGCACTGAAC
frmR	GAACGGGTCGTGCCATTCTAAATAG	GAACGGGTCGTGCCATTCTAAATAA	GCATTCAAAGGTATGGTCGATACC
b0361	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	GCTGCATCGTATACCCACAG
yaiS	CTTGCTGCATTAAAAAAACATAAAAGCTAG	CTTGCTGCATTAAAAAAACATAAAAGCTAA	AGTAGAGGGAATGCCGCC
tra5_1	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTA	CTGATGATAGCCTCAACGTTGATG
araJ	GCGAACCACTGGGTAG	GCGAACCACTGGGTAA	GACCGTTATATCAAACGTTGGG
pgpA	CCGCTGGGTATTCTGTCGTAG	CCGCTGGGTATTCTGTCGTAA	CGCAGAGCGGTTAACAGG

yajL	CGGCAGGGATTATAATTACGAGTAG	CGGCAGGGATTATAATTACGAGTAGA	GGGATTGATGTGGTTCTGC
panE	GCCTCGCCCCCTGGTAG	GCCTCGCCCCCTGGTAA	ACCAGGCAGCACGATCA
lon	TATGCAGGTTGTACTGCAAATAG	TATGCAGGTTGTACTGCAAATAA	CCTTACAACACCCCTTAATAAGGG
mdIA	AGGCCGTCGATGCGTAG	AGGCCGTCGATGCGTAA	TCAGGACCGCAATCCCC
ybaA	GATTGAGTCAATCATCGACGAATAG	GATTGAGTCAATCATCGACGAATAA	GCAGCGATTTGTGCTG
ybaJ	GAGAACCTGCGAGTTTATCTTGTAG	GAGAACCTGCGAGTTTATCTTGTAA	GCAATCGAAGTGGCGAAAAAAAT
prIC	GCGCGTTAACCGCTAG	GCGCGTTAACCGCTAA	GTATGTGCGTGAACTCGCGT
aes	CAGTTCTTACCGCTCAGCTTAG	CAGTTCTTACCGCTCAGCTTAA	TACGCCGATAACCAACGATTACA
ybcF	GGGACCTGTATTCGCTGTAG	GGGACCTGTATTCGCTGTAA	TGAAAAGTCCGCTGGTG
tra5_2	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTAA	CTACAGTTGAACCTAACTCACCTG
ybcL	CTGAGATAACACCAGTTATGAGATAAAGTAG	CTGAGATAACACCAGTTATGAGATAAAGTAG	TAATTCTCAATATAAAATTATAACCACAAGGAATAATAT
rzpD	CAGAAGTATATTAAATGAGCAGTCAGATAG	CAGAAGTATATTAAATGAGCAGTCAGATAA	CGATGCAGCTAAATTGTGGC
ybcY	TAATGTTTCCGCTTCAGGAAAAAAATAG	TAATGTTTCCGCTTCAGGAAAAAAATAA	GCTGAACCGTGTGATACATCAA
hokE	CGCTTACGAACCGAAGAAGTAG	CGCTTACGAACCGAAGAAGTAGA	ATCGGCACGTTAAATCATATCAGG
ybdL	GCCTCGGCCAGCTTAG	GCCTCGGCCAGCTTAA	TATTGCACTGGTATCAGAAAAAGGC
ybdM	GCGCCTGGACGGTAAATAG	GCGCCTGGACGGTAAATAA	GCGAGCGCACCAAGAC
rlpA	GTCATTTATTACTACCGCGCAGTAG	GTCATTTATTACTACCGCGCAGTAA	GCGACACAAGCATCGTTACC
ybeQ	AAATTCTGAGACTGAAGATTACTGTAG	AAATTCTGAGACTGAAGATTACTGTAA	GCACTGGTGGAACAGGC
ubiF	GCTGAAATATCGCTTAGGGTTGTAG	GCTGAAATATCGCTTAGGGTTGTAA	ATCGAATATGTCGGCAAATTCAAAC
ybfH	GAGGTCTGCTGATTGATAATGGTTAG	GAGGTCTGCTGATTGATAATGGTTAA	GTACATTTCATAGAAGGTATCTAAATCACCG
ybfD	GATGAGCTTATTGATTCACGTTGAATAG	GATGAGCTTATTGATTCACGTTGAATAA	CTTCAGTCGATGTAACTCATGAAGG
nei	CCTGGCTGCCAGCACTAG	CCTGGCTGCCAGCACTAA	TTTATGACTGCCTACCTCGCC
abrB	CGAACGGTCGGCCTAG	CGAACGGTCGGCCTAA	ATAAGCATCATGGGGCGCT
sucB	TCTGCTGCTGGACGTGTAG	TCTGCTGCTGGACGTGTAA	GTCAGCGTCGCATCAGG
bioD	AGTACATAAACCTTGCCTTGTGTAG	AGTACATAAACCTTGCCTTGTGTAA	CGGGAAGAACCTTGCCTTGTGTAG
moaE	GCGGCAAAACGCTGGTAG	GCGGCAAAACGCTGGTAA	CGTCAATCCGACAAAGACAATCA
ybhM	AAGGCATACCGCTTTTTCTATTAG	AAGGCATACCGCTTTTTCTATTAA	TTACTGGCAGGGATTATCTTACCG
ybhS	CCAAACGTCGGCTGGATTAG	CCAAACGTCGGCTGGATTAA	CTGTTGTTAGGTTCGGTTTCCT
ybiH	AAGGATTATCGCAAAGGAGTTGTAG	AAGGATTATCGCAAAGGAGTTGTAA	GTCATAGGCGGCTTGCG
ybiR	TTAGTTATCTCCGGCCAACTAG	TTAGTTATCTCCGGCCAACCAA	ATGAGCCGGAAAAGCGAC
yliD	CGCTGGATCCGAAATTAAAGGATAG	CGCTGGATCCGAAATTAAAGGATAA	AATAAAATTATCAGCCTTATCTTATCTTGTATAAA
yliE	TGGGATAAAAGTGGAAAATTAGTAAAAGAGTAG	TGGGATAAAAGTGGAAAATTAGTAAAAGAGTAGA	CAGCAATATTGCCACCGCA
ybjK	TTGAGAGGGTTGCAGGGTAG	TTGAGAGGGTTGCAGGGTAA	AACTTTCCGCAGGGCATC
rimK	GCCTGAAAACGGGTGGTTAG	GCCTGAAAACGGGTGGTAA	TACAACCTCTTCGATAAAAAGACCG
ybjR	TGGAGAAAATACGGGCAGGATTAG	TGGAGAAAATACGGGCAGGATTAA	GTGATGCTCGCGGGC

cspD	GAAGCGGCAGTCGCATAG	GAAGCGGCAGTCGCATAA	CAGTAAAGTGTGCGTGTCTG
lolA	TCACGGTAGATGATCAACGTAAGTAG	TCACGGTAGATGATCAACGTAAGTAA	CTGACCACCATAGCCACGG
ycaI	TGCCAGTGGATAACGGGTAG	TGCCAGTGGATAACGGGTAA	ACGCACAACAGTAATCAGTGC
lpxK	GCTGGCTCTGGCAACTAG	GCTGGCTCTGGCAACTAA	TTTGTATTCCAGCCCATTTCAG
ycbK	CAGCACGGCACTGGTAG	CAGCACGGCACTGGTAA	CAGAACTCATCTCTTTCCGGG
ycbX	GCACTTAAGTTGGCGCGTTAG	GCACTTAAGTTGGCGCGTTAA	TGTGGGTGCCCATGCC
tra5_3	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTA	TGTGACTCAGGAAAATGCCTAAA
yceO	GCAATTATGGATCTGATCTATGTGTTTATTTTAG	GCAATTATGGATCTGATCTATGTGTTTATTTAA	TTCAGCATCAGAGATGCTGGT
yceF	GAAAAACCCGCTGATGGGATAG	GAAAAACCCGCTGATGGGATAA	CCTGATAAGGCCTTACGCC
plsX	AGCGGAACCTCGCGGTAG	AGCGGAACCTCGCGTAA	CGCCGTTGCACTGATAATACG
fabH	CGCGCTGGTTCTGTTCTAG	CGCGCTGGTTCTGTTCTAA	GTAAAGGTGATTCGCTAATTCTACTG
pabC	TTTGTGAGCGCCCCGAATTAG	TTTGTGAGCGCCCCGAATTAA	CAGGCCTATCGACCG
b1146	AGACCGGATATCTATCCGAAAGATTAG	AGACCGGATATCTATCCGAAAGATTAA	TCGAAATTGAGAGATACAGCTCGT
ymfM	AGTTTCGTCGAAATTCAAGGGAAATAG	AGTTTCGTCGAAATTCAAGGGAAATAA	CGGCGGTGGAATGGC
ymfR	TCTGTCGGCGGAGGTAAATAG	TCTGTCGGCGGAGGTAAATAA	TATAGCCTATTGGATGCGTGG
tfaE	AACTGCCGGAGGCCTAG	AACTGCCGGAGGCCTAA	TCCTCTATTAAGAGGTTATCCGTACTC
ycgX	CTTTATATATTGAAGATGTAGAAAATAAAACCATTAATCTAG	CTTTATATATTGAAGATGTAGAAAATAAAACCATTAATCTAA	CAAATATCAAGTTGATAGTATTAGTCTGGTGAT
ymgC	AGGAATCCGTGCTCTTAG	AGGAATCCGTGCTCTTTAA	GAGAGCGAGAACTCTCCATTCT
ycgY	GGACTTGAACCAACCGTCTGTGTA	GGACTTGAACCAACCGTCTGTGTA	AGCGCTTACTCCGACAACG
hemA	GCCTCGGGCTGGAGTAG	GCCTCGGGCTGGAGTAA	ATGTTGTGAACGTTGTCCTG
b1228	GCTCGAGCGAACCTTAG	GCTCGAGCGAACCTAA	CGCTTCCCGATAAGGGAGC
kch	CAGTAAAGAATCGGCGAAAAATAG	CAGTAAAGAATCGGCGAAAAATAA	CAGCGCGGCGTTGC
sapB	CATAAGGAATGGTATGCCTTACGATAG	CATAAGGAATGGTATGCCTTACGATAA	ACATAGCGTGGGACAAACTC
pspF	CGTTGTTAAAAAGCACCAAGATTAG	CGTTGTTAAAAAGCACCAAGATTAA	AAAGAAAGCGTCCGGCC
ycjU	GGCCTTCTGGCAAAACGTATAG	GGCCTTCTGGCAAAACGTATAA	GATACAACGCGTAGTTCTGGAAC
ycjV	GTTGGGGGCACGAGTTAG	GTTGGGGGCACGAGTTAA	GTTCCTTCTCGGCCTGT
ycjG	ACGGGCGAATTGCATCTTAG	ACGGGCGAATTGCATCTTAA	GGCTCAGGCCTTGAATTG
ycjZ	GGCTGAAGTATAAGGTGCTGTTAG	GGCTGAAGTATAAGGTGCTGTTAA	CCCGTTTCCGGTATCATAATCAGC
intr	TTGAATGCGCGGTTATCGTAG	TTGAATGCGCGGTTATCGTA	TCTTGTATTTGTTGATTTCTGCATTATTC
sieB	GCAGGGAGTAGACGTTTAATCGTTAG	GCAGGGAGTAGACGTTTAATCGTTAA	AAAAGTGAACTTTAGATATAACACCTTATCAA
b1354	GAATCTCACATCTTGTGCTACGTATAG	GAATCTCACATCTTGTGCTACGTATAA	TACCCCATACCAACCCCCA
ydaY	AGCAGGATACGATAAAAAGCCATAG	AGCAGGATACGATAAAAAGCCATAA	GCCTGCGTCATTTGACTAATGA
b1367	GTATTTCAAGGAGCAGTGTGTTAG	GTATTTCAAGGAGCAGTGTGTTAA	TTTCATTAAGTTACGGACAAGAAATTCATATT
tfaR	GCCAGCACTGCCGTAG	GCCAGCACTGCCGTAA	GCATTGACCTGACCAGTCCA
paaG	CGCAGTTCACGGGAAATAG	CGCAGTTCACGGGAAATAA	AGACGCCGCTCAATGAC

paaX	AGGC GTTATGCCAATTATCAGATAG	AGGC GTTATGCCAATTATCAGATAA	ACCAATATGTCCATCTTCTCCTACAA
b1402	GGTTAAGTGATAACAGATGTC TGGAAATATAG	GGTTAAGTGATAACAGATGTC TGGAAATATAA	GTATATCTGAATGGAGATACGACAATCAG
ydcL	CACCATGTTGACGTTAACAAAAGTAG	CACCATGTTGACGTTAACAAAAGTAG	TACATTGAACAA CAGCAAACACCT
rhsE	AGGGAGTTCAGATGCTCAAATTATTAG	AGGGAGTTCAGATGCTCAAATTATTAA	TTTGAATTGTTATCAAACCCAAGGTAAC
yddJ	CCTCCAGTTCATGGCCTTTAG	CCTCCAGTTCATGGCCTTTAA	ATTAATCCCAAGAGCGCTCCC
ddpF	TGGCGGGCGCTGTAG	TGGCGGGCGCTGTAA	GGGATTGTGATTGGTATGATCCG
yddV	GAACTCTGGAAGCCAGTCTTAG	GAACTCTGGAAGCCAGTCTTAA	GAGTGATC GGGCTGCATAC
ydeV	GGAAAGCGCCTGGGTTATAG	GGAAAGCGCCTGGGTTATAA	GACATTAAAATGAAACTTATAAATTGTCAGAGG
ydeA	CACTCGAAGAACAGACGCAATAG	CACTCGAAGAACAGACGCAATAA	AAAGCAAGTCGGAAGAGCTG
marA	TTTTTACATCCATTAAATCATTACAACAGCTAG	TTTTTACATCCATTAAATCATTACAACAGCTAA	GTCGGGGCCAGAACAAAC
marB	GCCCTATTATAATCAACACGCTATGTAG	GCCCTATTATAATCAACACGCTATGTAA	GGACGCTATGAAACCTGGC
tfaQ	GCCAGCACTGCCGTAG	GCCAGCACTGCCGTAA	AGTATAAGTGC CATTGCCCG
ydfP	TGAATCTTAAGAGATAAAAAGCATCAAATGTAG	TGAATCTTAAGAGATAAAAAGCATCAAATGTAA	TTCTGATTAAGACCTTTATCTTACCCCTAAG
rzpQ	CAGAATGATTACATACCCGCGTTAG	CAGAATGATTACATACCCGCGTTAA	CGTGTCCGGCGCAC
b1578	GGTTAAGTGATAACAGATGTC TGGAAATATAG	GGTTAAGTGATAACAGATGTC TGGAAATATAA	AACGGCTTTGCTAAATTCTCCT
ynfA	TGGGGCGCACGTAG	TGGGGCGCACGTAA	CTGTGACCGGTGGTATGGC
speG	GAAGCCGACCGCACAATAG	GAAGCCGACCGCACAATAA	AATTACTGGATCTGAAAATAATACCGTG
dmsD	CGGTTAACCGCTGTTCGATAG	CGGTTAACCGCTGTTCGATAA	TCGGCCGAGCGCC
ydhM	CGACGCCTGCCGT TAG	CGACGCCTGCCGT TAG	ATGCCGC GTTACCCAGT
Ihr	AAGGGCTGGATTGGGATAG	AAGGGCTGGATTGGGATAA	AACTTGATGATTCTAATGCATAGAAGAAGAG
ynhG	GTTACCGTGACCGCAGTAG	GTTACCGTGACCGCAGTAG	GAAGCGCCCTGATGGG
sufA	GGCGAAAGCTTGGGTATAG	GGCGAAAGCTTGGGTATAA	TTCGCGATAAGTAGTGGCAAC
ydiA	CCTTAGTCGCCGAATGTACTAG	CCTTAGTCGCCGAATGTACTAA	ACGGGTGGCGTACTCC
ydiE	CAAGCTGCTGTTGACCAAGTAG	CAAGCTGCTGTTGACCAAGTAA	CATTGATGACTGGTTGCC
nlpC	GGCAGCGAGACGAATCTAG	GGCAGCGAGACGAATCTAA	GAAGGATGTTTCAGTATCCGGC
btuC	TGGTTATTGTTAAAAGCAGGACGTTAG	TGGTTATTGTTAAAAGCAGGACGTTAA	ACACTTGAGGCGACATTGAC
arpB_1	CACCCAACAGTAAATCTCAATGGTAG	CACCCAACAGTAAATCTCAATGGTA	AACGGAGGAGTAATGTTAATCAGGT
ydjX	ACTTACTCACCCAAAAAATGAAGGATAG	ACTTACTCACCCAAAAAATGAAGGATAA	CCAGCAACAGCCAGTAAACA
nudG	GCCAGACCAGCGGATTAG	GCCAGACCAGCGGATTAA	GTCAGGGCATTGTAAGGTTG
b1788	ATCGAACGGACCGGCTAG	ATCGAACGGACCGGCTAA	TATCGCGCCGAGAAAGA
yeaL	GCTGATTGTGGGAAACAGTAG	GCTGATTGTGGGAAACAGTAA	GGTTTGGATACCGGGCG
yeaX	CGCCTGGTGGATTGTAG	CGCCTGGTGGATTGTAA	GTGAACTTGCTGCGTGA
yobB	GGCGATATCATTCCATTACGCTAG	GGCGATATCATTCCATTACGCTAA	TATAACGCCATATTGCTGTACTTGATC
exoX	TTAACACTGAAACATTATCTGGAAAATACTTAG	TTAACACTGAAACATTATCTGGAAAATACTTAA	TATGACAACGTCACCGCACA
yeC	GTTGGTTTCTCCCTGCGTTAG	GTTGGTTTCTCCCTGCGTTAA	AGATCGTAAACCTGCGTACCA

otsA	ACCTTCCAAAGCTTGCCTAG	ACCTTCCAAAGCTTGCCTAA	CCTACGGTGAGTTAACGCAAC
dcyD	GCCTATCATCCCCACGTTAG	GCCTATCATCCCCACGTTAA	TAAACCGAGCAGTAAGCCA
yedM	CCCACCCATTGGCATAAATTAG	CCCACCCATTGGCATAAATTAA	GAAACCTTGCAAAGCTGGAATC
fliE	GTGATGAGCATGCAGGTGAG	GTGATGAGCATGCAGGTGAA	TTTTTTTGAAAGTCATTGATGCGC
fliN	GCCGCCTGAGCCGTTAG	GCCGCCTGAGCCGTTAA	CGATCACCGGTGACATAATAAAAAG
fliP	GCGCAGAGCTTTACAGCTAG	GCGCAGAGCTTTACAGCTAA	GCGGTTCGCACAGCG
fliQ	CCTGCCGTATATCATCGGGTAG	CCTGCCGTATATCATCGGGTAG	CAGGGTGTAAAGGTATCGAC
yedS_1	CGTAACAATGGCTCTTGGTTAG	CGTAACAATGGCTCTTGGTTAA	TCACCATTATCAAACCTGCCAC
cbl	GCAGTGAAGAGGAAATTGATTACAGATATAG	GCAGTGAAGAGGAAATTGATTACAGATATAA	ATAATGAGGGAGAACATCAGCAAAGC
b1996	GGTTAAGTGATAACAGATGTCCTGGAAATATAG	GGTTAAGTGATAACAGATGTCCTGGAAATATAA	AAAATCAGCAACGAAGAGACGC
hisL	CCATCATCACCATCATCCTGACTAG	CCATCATCACCATCATCCTGACTAA	AGCTATGCGTAAACGAGTGTG
wbbJ	TGAGACCAAATTATGGGAAAAAGCATAG	TGAGACCAAATTATGGGAAAAAGCATAA	CTCTTAGCAGAACGACTATGCG
wcaM	GCCGGAACGTAGGGAGTAG	GCCGGAACGTAGGGAGTAGAA	GTGATGTTACGCCGCTTCG
wcaL	AGCTTGCTGCAGGCTTATAG	AGCTTGCTGCAGGCTTATAA	ACGAATAACAAAATGTTACCATTTCACAA
wcaC	GAGTATGTCAACTTCTATCAGAACATCTGAG	GAGTATGTCAACTTCTATCAGAACATCTGAA	TTGAAATGCCCACTCCAGC
asmA	GAAGAAGTTGCTGGAGAACGATGTAG	GAAGAAGTTGCTGGAGAACGATGTAA	AAGTGGAAAGAGATCGACGCC
baeR	GCCTGCCGCATCGTTAG	GCCTGCCGCATCGTTAA	TAACGGAGGCAATTCCGGT
gatR_1	CGCGGGTAAAATTAAATTACCGGTGAG	CGCGGGTAAAATTAAATTACCGGTGAA	AGGCCGGTGGCGG
tra5_4	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTAA	CGTCTTGTTCAGGATCTGG
yegV	TCCTCGCACACAAAAACGTATAG	TCCTCGCACACAAAAACGTATAA	TAATTCATGATGTTGATGCCATCGG
yegW	CGTTTTGTGTGCGAGGAGTAG	CGTTTTGTGTGCGAGGAGTAGAA	TCCGGCAATTCCAACGC
yehQ	AGAGTGTATTGGTCAGGCATAG	AGAGTGTATTGGTCAGGCATAA	ATTGTTCGCAAAGCAAAACACC
yohC	GGCTACGGTTATCGTTGTTCTAG	GGCTACGGTTATCGTTGTTCTAA	CGATCGTCAAAGGAGAACGTG
yohF	GAATCCACAGTTCAACCCAGAACATAG	GAATCCACAGTTCAACCCAGAACATAA	TTGTGATTATTTTGTTCGCCATG
sanA	TTACTTGAATTACAAAAGAACAAAGGAAAGTAG	TTACTTGAATTACAAAAGAACAAAGGAAAGTAA	GGCACACTCTGGCACAAAC
yejA	GCCAGCAAACAGGGAGAGTAG	GCCAGCAAACAGGGAGAGTAGAA	GAAGAAGACAATCAGCAGGATGG
yejE	CATTGATCCTAATAAGGCCGTGAG	CATTGATCCTAATAAGGCCGTGAA	GAGAGCTGATGCGGATAATCTG
b2191	GTAAATGCCCTGAATCAGCCTATTTAG	GTAAATGCCCTGAATCAGCCTATTTAA	TTTGTCTCAGCCGATGCC
rscD	CAGTTATGTCAAGAGCTGCTGTAG	CAGTTATGTCAAGAGCTGCTGTAA	TCAGAACAAATGATCGACAGGCT
rscC	GGAAATCGCGGGATTCTGTAG	GGAAATCGCGGGATTCTGTAA	AGTGACCTTAAGTCCGGCAG
yfaT	CGTTAAATTCTGGCGCGATAG	CGTTAAATTCTGGCGCGATAA	CCGATAATCACGCCCG
menF	GCTCGTACTTATTACAAATGGAATAG	GCTCGTACTTATTACAAATGGAATAA	CCGCCAGCGTCGG
yfcO	GTTCCAGTACATACTGAATGAGTTGTAG	GTTCCAGTACATACTGAATGAGTTGTAA	GAGGAGTTGAGCGCGTTG
yfcU	GGGCGGATAAGGGCATGTAG	GGGCGGATAAGGGCATGTAA	TCATCAGGAACAACCGGCG
tfaS	CTGAAC TGCCGGAGGAGTAG	CTGAAC TGCCGGAGGAGTAGAA	CCGGTTAATTATTCAATGGGGC

ypdI	CGAATTATCTTATTCATCCTGTGCGATAG	CGAATTATCTTATTCATCCTGTGCGATAA	TAAAGAGTGTAAAGACTAGTCAGGACATAA
yfdY	GGGTATGGCAGGCGGTAG	GGGTATGGCAGGCGGTAA	CGCAGAGAACTATTCTTATATACCACAAA
yfeO	CCACCCCACGATAACGTTAG	CCACCCCACGATAACGTTAA	CACGATAGCCACGCTCATAC
mnhH	ACGGCGCTGGGATTGTAG	ACGGCGCTGGGATTGTAA	CAAAAACGTTGGTGGCGT
xapR	TTGGCTGCATTGACACAGTAG	TTGGCTGCATTGACACAGTAA	TCTCGCATACTCAAAGATTGCAAC
yfeR	AAGGGGATCCGTTGTATCAGATATAG	AAGGGGATCCGTTGTATCAGATATAA	GAATGGCGCAGTTGCACT
yffB	TATCAGCAATTTCATGAGGTGTAG	TATCAGCAATTTCATGAGGTGTAA	AACGGTAAAACCGATGCC
hda	CGTTTGAAAGAAATTCTGAAGTTGTAG	CGTTTGAAAGAAATTCTGAAGTTGTAA	CGAATACTATGGATTAACCTCGCTAG
yfgG	CGAACACCGGTACAACGTTAG	CGAACACCGGTACAACGTTAA	TAGCTCTTCAGGACATTGGTATT
pbpC	CGACAGTGAATTGTATGCAATAG	CGACAGTGAATTGTATGCAATAA	AAACGCCCCGGTGAGC
yphA	CAATTCTCTCGATCGGCGTTAG	CAATTCTCTCGATCGGCGTTAA	GGGTAAGTCAGGCGTTCTTAA
yfhB	GTGAACTCCAGCACTGGAATAG	GTGAACTCCAGCACTGGAATAA	CTCATCCGCCAGTATTCTTC
kgtP	GGAAGGGATGCGTCTTAG	GGAAGGGATGCGTCTTAA	AGCCGCATCTGTAATCACA
yfiA	CGTCGAAGAAGTTGAAGAAGAGTAG	CGTCGAAGAAGTTGAAGAAGAGTAA	GCCAGTAACGGGTTTCCG
yfjQ	GCTCACGCACTGCAGTAG	GCTCACGCACTGCAGTAA	TTCTGCCTGTGTCATGAGAGAT
yfjR	CGACAGCCCACCGGAATAG	CGACAGCCCACCGGAATAA	ACTGGCAGCACCGGC
ypjC	GTTTTTGAAATGCGCTAAAGAAATGAATAG	GTTTTTGAAATGCGCTAAAGAAATGAATAA	TATGAATTACGTGATTCCATACAGACATT
ygaQ	CAGACAGGATAGGAGAAAGAAAAACATAG	CAGACAGGATAGGAGAAAGAAAAACATAA	TGTTCAGCACGACCATACTGATA
ygaR	AAGGTGGTATCCCTGGCTATTAG	AAGGTGGTATCCCTGGCTATTAA	TAGGTAGAGCAACCTTATAAGCTACG
yqaC	CGGCGGTGAGGCGTAG	CGGCGGTGAGGCGTAA	AAAAAATATCTACATTCTGAAAATGCGCA
gabT	TTTGATGAGGCGAAGCAGTAG	TTTGATGAGGCGAAGCAGTAA	CGGGCGATTTGGCTT
ygaU	GTTGCGTATTCCGGAAGAGTAG	GTTGCGTATTCCGGAAGAGTAA	AGGGTATCGGGTGGCG
ygaM	GTTAACATGCGCAAATCGTAG	GTTAACATGCGCAAATCGTAA	CGCAACGCTTCTGCCG
luxS	GTTGCAGGAAC TGACACATCTAG	GTTGCAGGAAC TGACACATCTAA	ATGCCCAAGGCGATGTACA
mltB	GCTGGCGCGAGTACAGTAG	GCTGGCGCGAGTACAGTAA	AGACTCGGCAGTTGTTACGG
srlE	GGTTTGCTCCGGTTTATCTATCAATAG	GGTTTGCTCCGGTTTATCTATCAATAA	GGATGGAGTGCACCTTCAC
norW	GATTGTTGAAAACATTGCCGATGTAG	GATTGTTGAAAACATTGCCGATGTAA	GTGTTGCATTGGACACCATTG
ascB	CCAGTAATGGGAAGATTAGAGTAG	CCAGTAATGGGAAGATTAGAGTAA	CGCTTATCGGGCTTCATG
hycl	AGTTAGCGGTGGAAGAAGAGTAG	AGTTAGCGGTGGAAGAAGAGTAA	TGGGCGGCCTGG
hypB	GAGACACAGCGATGTGATAG	GAGACACAGCGATGTGCATAA	TTTGCAGGTTGGATTCTCCT
ygbA	TATCGTCCGAAAAAACCTCATGAATAG	TATCGTCCGAAAAAACCTCATGAATAA	GTGCGCTAATCGCCGC
pphB	GGCGGCTGTCTTTATAAAATAAGTAG	GGCGGCTGTCTTTATAAAATAAGTAA	ACTGACTGTGGTCACAAACGA
ygcN	AGGAGTCTGCGATGTCTGTAG	AGGAGTCTGCGATGTCTGTAA	CGTACAACACGGAATAATTGGC
mazF	GCCAAAATTAAACGTACTGATTGGGTAG	GCCAAAATTAAACGTACTGATTGGGTAA	AACACCACCTGGAATAGCAGAT
relA	TCGGTTGCACGGGAGTTAG	TCGGTTGCACGGGAGTTAA	CGGGCTTTACGCACTG

rumA	GTACTTTCTCGCGCGTAAATAG	GTACTTTCTCGCGCGTAAATAA	CAGACAATACGCCAGGTTTC
ppdC	CATTGCCGAATCGTCAGTAG	CATTGCCGAATCGTCAGTAG	ACTTTGCACCAAGAACATCTCTG
ptsP	CTGATTCGCGGAGGGTTATAG	CTGATTCGCGGAGGGTTATAG	GCTCAAAGGTGCGAATAATAGC
mutH	CCCGTCATTTCTGATCCAGTAG	CCCGTCATTTCTGATCCAGTAG	GTAAAAGGAGTGAGTACGCCCT
ygeA	TGTCGCTTTATGCTGCGTAG	TGTCGCTTTATGCTGCGTAG	TCAGCGCCGAGAAAGT
kdul	GCCGTTAAAGATTGCGCTAG	GCCGTTAAAGATTGCGCTAA	TAACATTAATGTTGTTAGCCCATT
yqeF	TTGACCATTGAACGTGACGAATAG	TTGACCATTGAACGTGACGAATAA	CAACTCCCCGCCAACG
ygel	CTATCTCACCTACTATAAAATTGAGTGGTAG	CTATCTCACCTACTATAAAATTGAGTGGTAG	GTTCATCTTTATTATTCCACGTTTTAACAG
pbl	CAAATATATATTGTATATACCAGGCTTAATGAACTAG	CAAATATATATTGTATATACCAGGCTTAATGAACTAA	CTTCAGGTATTCCTGATAATCAAC
ygeM	GGCAAGCCCTGAGGACTTATAG	GGCAAGCCCTGAGGACTTATAA	TTCCCATATATTCTGACTGAGTGTAAATG
b2860	GGTTAAGTGATAACAGATGTCGGAAATATAG	GGTTAAGTGATAACAGATGTCGGAAATATAA	ATCGTGCCTTTCATTTATTCCAG
ygeP	ACACCAGAAGAAAAGAGCAAGTTAG	ACACCAGAAGAAAAGAGCAAGTTAA	CCGCTCGCTTTCTCCG
yqeC	GCGCGCAGATTGTGAATTAG	GCGCGCAGATTGTGAATTAA	TCGAGTTTGCAGCCTCTG
ygfJ	AGCGAAGGAAAGGTATACTGAAATTAG	AGCGAAGGAAAGGTATACTGAAATTAA	GATGAACGTGTCATCGCCG
recJ	TCATCGACAATATCTGGCCAATTAG	TCATCGACAATATCTGGCCAATTAA	CTGTACGCAGCCAGCC
argO	TGCACAAGCCTGTTAGTTAG	TGCACAAGCCTGTTAGTTAA	AATCGCTGCCTACGCG
yggU	CAGAAATCGCGCGTTAATTATTAG	CAGAAATCGCGCGTTAATTATTAA	TAACCAAAGCCACCAAGTGC
mutY	GGCGCGCCGGTTAG	GGCGCGCCGGTTAA	CGCGAGATTTTCATCATTCCG
glcC	GCTGGAGATGAACCTGAGTTAG	GCTGGAGATGAACCTGAGTTAA	GGGCAAATTGCTGTGGC
yghQ	CTCGAAGCGTATGACCTGATTAG	CTCGAAGCGTATGACCTGATTAA	ACCAACTGGCGATGTTATTAC
yghT	CGCGCGTGGTTACTAG	CGCGCGTGGTTACTAA	GACGATGGTGGTGGACGG
ygiZ	TGGGGACGGTTATATTGCTATTAG	TGGGGACGGTTATATTGCTATTAA	ATGCCAAATTGCATGGCA
yqiB	CGATGGCGATTCCGGTTATTAG	CGATGGCGATTCCGGTTATTAA	AAAATCCTGACTCTGGCCTCA
b3045	GGTTAAGTGATAACAGATGTCGGAAATATAG	GGTTAAGTGATAACAGATGTCGGAAATATAA	CGTTTGTGCGACACCCG
yqil	GACGTAATCCTGAAAATCACCTATAACTAG	GACGTAATCCTGAAAATCACCTATAACTAA	ATGACCTGTGGTTATAGAACATATAATGG
ygiP	GATGAAGGCTATCAGGTATGAG	GATGAAGGCTATCAGGTATGAA	TCCAGTGCCTCTGGTTT
yhaK	CTTGCTGATAGATTGCGCTGTCTAG	CTTGCTGATAGATTGCGCTGTCTAA	AATGGCGCTGGATGATACC
tdcA	ACGAAGGCAATTAAAGAGTTGGTAG	ACGAAGGCAATTAAAGAGTTGGTAG	GGGAAACCCCTTGCAC
yhaC	CGTATGATTACGACCTTTAAATGCAATATAG	CGTATGATTACGACCTTTAAATGCAATATAA	CGTAATAACCGTCCGGCG
ecfH	GTAACTACGGCGTTACGTTATTAAATAG	GTAACTACGGCGTTACGTTATTAAATAA	CACTGATTATGCTGCGCAAAG
yhbW	GATGTTAAGGAAGAGTTGGGATAG	GATGTTAAGGAAGAGTTGGGATAA	GCAACGCACTGGTGCATAT
nlpI	GCAGAACGGACCAGCAATAG	GCAGAACGGACCAGCAATAA	TGAAATTGATCAGCAATTTCATTGAAAAG
dacB	GCCGTTGTATAAGATATTATCAGAACATTAG	GCCGTTGTATAAGATATTATCAGAACATTAA	GCATAAACAAAGCGCACTTGT
ptsN	GGTACTCCGGATGAAGCGTAG	GGTACTCCGGATGAAGCGTAG	CCAGTTGCTCTGCAATACACC
yhcC	GGCTACCTCCAACGGAGTAG	GGCTACCTCCAACGGAGTAG	CAGTTGTTTCGCTTTCCGG

yhcE	GTAAATGCCTTGAATCAGCCTATTTAG	GTAAATGCCTTGAATCAGCCTATTTAA	CACCCAGCTCGACCAAGA
yhcO	CATTGCGTTTAATGTCGTCATTAG	CATTGCGTTTAATGTCGTCATTAA	CTTTTTGTTATAAATTACATTTAACACTTAGTATC
mreC	CGCCGGAGGGCAATAG	CGCCGGAGGGCAATAA	GACGTTAATCACTAAAACCTGCC
yhdN	GTTGTTGGACAAATCAACGATAACTAG	GTTGTTGGACAAATCAACGATAACTAA	CCTGCACAATGCCTTTGACT
kefB	CGGCTGGGATGAATTGAGTAG	CGGCTGGGATGAATTGAGTAGAA	AAAACTCGGCGCATATCGC
frlD	ACCACGGTGCTGGTAG	ACCACGGTGCTGGTAGAA	AACCCCTGCGCGATAT
bioH	CGTTGAAGCAGAGGGTAG	CGTTGAAGCAGAGGGTAGAA	CTGCATATAGCAGAAATAATGCTGAATC
gnrX	GTGCCCTTGTGCAACCTTGAG	GTGCCCTTGTGCAACCTTGAA	GCATCGGAAATACGGATCATAGTAAT
maiQ	GCTGCAGCGAAGAAGAAGTAG	GCTGCAGCGAAGAAGAAGTAA	TCGATAAGCCAATTCCCGAAG
glgA	CGTGAGCTTACTATCGCTTGAATAG	CGTGAGCTTACTATCGCTTGAATAA	TCTGATCGTAAGCGACTCCC
yrhA	TGATGCTGCCAACTTACTGATTAG	TGATGCTGCCAACTTACTGATTAA	CTGATTACGTGCAGCTTCCC
ugpQ	CCGAACCTTACGGCCCAATAG	CCGAACCTTACGGCCCAATAA	TTTTGTCGGGAAGCGAGTAAAC
gadE	CACCCGGGTATCACATCTTATTTAG	CACCCGGGTATCACATCTTATTTAA	ACAACGGTATTAACAGCTTCTTCTT
gadX	CGTTCTCGGAAGGAATAAGATTATAG	CGTTCTCGGAAGGAATAAGATTATAA	TGGTAGGACCAAAATTATCCACAAAG
yhjK	GAAGAGAGTTACCTGGAAGAAAAGTAG	GAAGAGAGTTACCTGGAAGAAAAGTAA	AGGACCTGAAAGTAAAGGCTTTAAA
yhjR	CAGAGTTGCGCAACAAAAGTAG	CAGAGTTGCGCAACAAAAGTAA	GACGGTGGTAAATCAACATTAATG
yiaG	GCATTAAGTAAGCAGTTGATGGAATAG	GCATTAAGTAAGCAGTTGATGGAATAA	GTTGATGTGCATTAAGCCACG
xyIR	GATGTAATAGCGAGGTGATGTTGAG	GATGTAATAGCGAGGTGATGTTGAA	GGATAAGCGTTACGCC
sgbU	GCAGGGAGGCTGGATTATGTTAG	GCAGGGAGGCTGGATTATGTTAA	CGGTTAATGACGTTGGCTATTTC
rhsA	CCAGACAGTCAAACGATAAAAAAAAGATAG	CCAGACAGTCAAACGATAAAAAAAAGATAA	GGAAAGTCCGATTATTGCTTCATAC
yibA	GCTATTGATAAGCTGAAGCGTCATAG	GCTATTGATAAGCTGAAGCGTCATAA	TGAAAACGCCCTGGATATTATCTC
lctD	CGAAAGGGAATCGGGCATAG	CGAAAGGGAATCGGGCATAA	CGCCATCCTGATAGCTTACG
yibK	CGGGAGCGGTATTGAGAGATTAG	CGGGAGCGGTATTGAGAGATTAA	AACGGCGGTGATTGAAAACG
yibD	TAGGCCCTTAATTGCGCTAG	TAGGCCCTTAATTGCGCTAA	TAACCTGCCGCCAGACATTA
htrL	CGCTGAGAATTTCCCTTCAAGAAAATAG	CGCTGAGAATTTCCCTTCAAGAAAATAA	CGCGACGAGATAACGCG
coaD	CTGATGGCGAAGTTAGCGTAG	CTGATGGCGAAGTTAGCGTAA	GATGGTAAACCGGGCTATTTCG
rph	GAGGGGAATCGAATCCATTGAG	GAGGGGAATCGAATCCATTGAGAA	AAATTCAATAAACTGGCGCTGATATG
dinD	GGAAAACAGTGTAAAAATTACAGAGAGAAATAG	GGAAAACAGTGTAAAAATTACAGAGAGAAATAA	CACTGCACCTGGACCTTG
ligB	GCAGATCACAGGTTGACCTTAG	GCAGATCACAGGTTGACCTTAA	AAATATTGCACCTTCTTTCCCCC
setC	ATGATTGCGCTGCTGTTATTAAGATATTAG	ATGATTGCGCTGCTGTTATTAAGATATTAA	AACGTGCCATAGCGGGC
yicO	GCAC TGAAAGATTATTCTGGTGGATTAG	GCAC TGAAAGATTATTCTGGTGGATTAA	TGCGGCGTGAAACGTCT
ivbL	CGGCAATCGGCCGTAG	CGGCAATCGGCCGTAA	TGTC CACTTCTGGAGGC
yidH	CTGGTGTGATGCCGGATAG	CTGGTGTGATGCCGGATAA	CTTCAGCATCAATGACCTGACTTC
glvC	GGCGGAGGTCTGATTGACTAG	GGCGGAGGTCTGATTGACTAA	ATTGCCGACCCGCC
yidS	GCACATATTCCACAGTTGAAGGATTAG	GCACATATTCCACAGTTGAAGGATTAA	TTACCTGGTCGCTGGTTCT

yieH GTGGTTGGGATATTACGGCATAG
yieJ GACTGTGGGGTGA~~TTTT~~CGTAG
atpE GATGTTCGCTGTCGCGTAG

GTGGTTGGGATATTACGGCATAA
GACTGTGGGGTGA~~TTTT~~CGTAA
GATGTTCGCTGTCGCGTAA

CAGCGGTTCTTGCGAAGA
CAGCTGCATCCTCGCTG
ATTGTTGC~~G~~T~~A~~AGATT~~C~~ACAGCA

Table S13. Sequences of MASC-qPCR primers

Gene	MASC-qPCR_forward_TAG_primer	MASC-qPCR_forward_TAA_primer	MASC-qPCR_reverse_primer
rbsB	ATCTGAAACTGGTTAAGCAGTAG	ATCTGAAACTGGTTAAGCAGTAA	GGTCAGCATTAATGCTGCCA
rbsR	GAACCGCGGTCGGCTTAG	GAACCGCGGTCGGCTTAA	TTAGGCCTTGCTGTAAGTGC
ilvL	ACTTGGACGAGGAAAGGCTTAG	ACTTGGACGAGGAAAGGCTTAA	TGCCCGCAACGCATG
ilvA	AGGTCTTTGGCGGGTTAG	AGGTCTTTGGCGGGTTAA	ACCGCGTGTGATTAGAGC
wzzE	CCGCGTTCGTCGAAATAG	CCGCCGTTGCTCGAAATAA	CATCTCCCGATGCTGCG
asIB	CATTGCTGGTGGTAGTAAGTAG	CATTGCTGGTGGTAGTAAGTAA	CAGATTAAATCTGACTAAGCCGC
hemY	CAGAATAACCCGCCACAGTAG	CAGAATAACCCGCCACAGTAA	GCTTATCGTCACTGACAGATG
yigG	TGCACCTACTGATTCATCAAACAATAG	TGCACCTACTGATTCATCAAACAATAA	TTGAATAGTTAACGCTTGCTTACTTTAATG
recQ	TGATGGCGATGACGAAGAGTAG	TGATGGCGATGACGAAGAGTAA	TCGTTCTTACGGAACGA
rmuC	GAATATAATCAGCAGTCGCGCTAG	GAATATAATCAGCAGTCGCGCTAA	CGTGGCGACCATAATCCG
tatD	CACTGTTGGGATTGCGTTTAG	CACTGTTGGGATTGCGTTTAA	CATTGTCGATCCGGCAACC
yihL	CCGTAGACCTCATTAATCTGTAG	CCGTAGACCTCATTAATCTGTAA	ACATGGATTTGACGCCACG
yihW	CCCCAGGAAGACCGTAG	CCCCAGGAAGACCGTAG	ACCGCTTAAATCGCTCCAG
yiiD	GCGGGAACGAAGAAGAGTAG	GCGGGAACGAAGAAGAGTAA	GATGATGAATTAAAGCATTATCGCGATAATT
cpxP	TAGCAACTCACGTTCCCAGTAG	TAGCAACTCACGTTCCCAGTAA	ACTGACCAGCGCTCCATAAG
frwD	GCAAACCCATCTTATTCTGGAGTAG	GCAAACCCATCTTATTCTGGAGTAA	CGACTGGAGCACGCTAAAGA
zraR	TGGCAAAACTGTCGCGTTAG	TGGCAAAACTGTCGCGTTAA	AAAATGGCGGATGACGAG
yjaB	GCGTATGTGGGGCGTAG	GCGTATGTGGGGCGTAG	CGCATTCTCCATGAAGTGGTC
yjdK	ATGACTATTCGTCAGTTTACAAGTAG	ATGACTATTCGTCAGTTTACAAGTAA	CAGACTCATTGGCAGGTTATTTC
blc-	GGTACAGCAGCCTGGTAGTTAG	GGTACAGCAGCCTGGTAGTTAA	TTGCCTGGCGATGAAATC
ulaF	CGCTTATTACGGGCAGAAGTAG	CGCTTATTACGGGCAGAAGTAA	ACCGGGGAGTAACGGC
yjfY	CAGCGCGGATATTATCGCTAG	CAGCGCGGATATTATCGCTAA	ACACTCATGCGTAAACACGG
priB	CAGATTGAATTGATAGATTCTGGAGACTAG	CAGATTGAATTGATAGATTCTGGAGACTAA	CCAGCTGACGCTGGTATTTC
ytfB	AGTTTATTCTGTCGCGGTAG	AGTTTATTCTGTCGCGGTAA	AGATATCGACCCATTGCAAGGT
ytfG	GCGTAAGCCATCTTAAATGTTAATAACTAG	GCGTAAGCCATCTTAAATGTTAATAACTAA	CGACAAAAATAAGCCCCCACA
msrA	GCGCCCGGAAGCATAG	GCGCCCGGAAGCATAA	CAGAGGGTAAAATTAGACAGCTG
ytfN	GGATTGCTCTATCAGTCGAGTTAG	GGATTGCTCTATCAGTCGAGTTAA	CGATAAAACTCACCGTGACCG
b425	TCGTGATGATCGTCGGTAG	TCGTGATGATCGTCGGTAG	TCAGTCACACATTGTCGCG
idnR	ATCACGGCAACACGCTTAG	ATCACGGCAACACGCTTAA	AGTTTTGCAAGCTAACGGT
b427	GGTTAAGTGATAACAGATGTCGGAAATATAG	GGTTAAGTGATAACAGATGTCGGAAATATAA	GGTTTTAAGGGAGAGAGGAATATACC
yjgX	CGTGTGACAGCCTTAACCTCTAG	CGTGTGACAGCCTTAACCTCTAA	AACAGGATTGGCACTGTCG
b428	TGGAGAATGAAATTAAAAAGGCTACTGTAG	TGGAGAATGAAATTAAAAAGGCTACTGTAA	AAATGGGCTAATTGGCAGTAC
fecE	CCGATGTGCTTAATGAGGTAG	CCGATGTGCTTAATGAGGTAA	CAAGCCTGTACAGCTCTGGT
nanC	GCATTGGTGTGTCATTTAAACTGTAG	GCATTGGTGTGTCATTTAAACTGTAA	CATGCCGTACCTGCGC
fimB	ACAGCGTCACGCTGTTTATAG	ACAGCGTCACGCTGTTTATAA	TTATTATTGAAGAACATAAACCATGTATTGTATG
yjiN	GTTCCCCCTCGGCAATTTTAG	GTTCCCCCTCGGCAATTTTAA	GCCTGTCTGGCAGGCT
yjiP	CTATTCATGGCGGTGATGTAG	CTATTCATGGCGGTGATGTAA	GCACGACAGTAACATCCACC

mcrB	GACCAACAAATTATTAGGGGACTCATAG	GACCAACAAATTATTAGGGGACTCATAA	AGCCCTCGCGTGAAA
yjjQ	ATTAAGAAGAGAAATGTCGCACTCATAG	ATTAAGAAGAGAAATGTCGCACTCATAA	TCTCTCGCCTCACTTCTCAT
yjjV	ATACGTTTTAACGTGCCGTAG	ATACGTTTTAACGTGCCGTAA	CATGATAAGACGCCACAAGCG
IplA	CGGGGGCTGTAAGGTAG	CGGGGGCTGTAAGGTAA	AGGTGAAGTTGATCTAACGTCAG
creC	GACTTCACCGTCACTTCACATAG	GACTTCACCGTCACTTCACATAA	ATCGCTACGGTAATCAGCACG
kefF	CAGGAGGCCCATGGATAG	CAGGAGGCCCATGGATAA	CCCCAATCTCGCAAAGTG
yabI	GCGTAAAGTGGTGGGTTAG	GCGTAAAGTGGTGGGTTAA	GTATGACCAATGAGTTGAGCG
thiQ	CACTATTGGGGATTACGGGTTAG	CACTATTGGGGATTACGGGTTAA	TTAATTGCGCACCGTTGAT
murF	CTTACAGGAGAATGGGACATGTTAG	CTTACAGGAGAATGGGACATGTTAA	CGTCGTTACGCACCAC
mutT	TTGCGAAGCTTAAACGCTGTAG	TTGCGAAGCTTAAACGCTGTAA	GACAGCGTCGCATCAGG
pdhR	CGTCTGGAGCAACGAAAGAATTAG	CGTCTGGAGCAACGAAAGAATTAA	GGAAACGTTCTGACATGGGTTATT
sfsA	AAATCACTGCCGTTACATTGTAG	AAATCACTGCCGTTACATTGTAA	TTGCTCTCTAACACGCAC
btuF	AATGCGCTTACAGGTAGATTAG	AATGCGCTTACAGGTAGATTAA	GAATTGTCCCGCCGCC
cdaR	TACAACGGATGAAGAGCGGTAG	TACAACGGATGAAGAGCGGTAA	TCCTCGACGACTTACGTCAC
yaeI	ACGATGCTGGAACGGTAG	ACGATGCTGGAACGGTAG	TTTCAGATTGTCGACATAGCGTTAC
yafL	TTTGACGGAAGAGACGATTGTAG	TTTGACGGAAGAGACGATTGTAA	GGCGACTCCTTTCTCAACG
yagY	GGTGATAAGTTATTCCCGTGAATAG	GGTGATAAGTTATTCCCGTGAATAA	GGCCTGACTGAAGGC
eaeH	AGTGCCTTACCCAGCAATAG	AGTGCCTTACCCAGCAATAA	TGATTACATACAGGCTGAGTTAC
b029	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTAA	AATTAAAGACGGATATCTATTGTTCCA
yahL	ACGTTAAATCCGCTACACTCTTAG	ACGTTAAATCCGCTACACTCTTAA	CTGCGAAACCACTACTGGTG
yahM	CGGCAAATCAGGTTGATTACGTAG	CGGCAAATCAGGTTGATTACGTAA	CGCATCAATTATCTGGCGAGTT
prpE	GCCAGGCGATGGAAGAGTAG	GCCAGGCGATGGAAGAGTAA	TGGGTAGGCCTGATAAGACG
cynR	GGCGGAAATGAATCACGGTAG	GGCGGAAATGAATCACGGTAA	AACAACCGCGCATTCTC
frmR	GAACCTGGTCGTGCCTATCTTAAATAG	GAACCTGGTCGTGCCTATCTTAAATAA	GGGTAAATGCGTCGGTATGG
b036	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	GAAGCTTAATGTTAAAGAGAAAAATATTGAGTT
yaiS	CTTGCTGCATTTTACATAAAAGCTAG	CTTGCTGCATTTTACATAAAAGCTAA	CATAGCAACATTGCTATGGACATACA
tra5	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTAA	CTAAATTAACTTCAGATACTATCGATTAAACTAACG
araJ	GCGAAACCACTGGGTTAG	GCGAAACCACTGGGTTAA	AAAAGGTGCCAGAACCGTAG
pgpA	CCGCTGGGTATTCTGCGTAG	CCGCTGGGTATTCTGCGTAA	ATCGGAACCTCGCGCGA
yajL	CGGCAGGGATTATAATTACGAGTAG	CGGCAGGGATTATAATTACGAGTAA	CGATCTGACCAGAACAAAACC
panE	GCCTCGCCCCCTGGTAG	GCCTCGCCCCCTGGTAA	ACCAGGCAGCACGATCA
lon-	TATGCAGGTTGTACTGCAAAATAG	TATGCAGGTTGTACTGCAAAATAA	TGAATCCTCAAGGTACGAACG
mdIA	AGGCCGTCGATGCGTAG	AGGCCGTCGATGCGTAA	ACCACTTCAACGGCAGGT
ybaA	GATTGAGTCATCATCGACGAATAG	GATTGAGTCATCATCGACGAATAA	AGCGGAGGGAAATCGAAACC
ybaJ	GAGAACCTCGCAGTTATCTGTTAG	GAGAACCTCGCAGTTATCTGTTAA	GGTGATCTGCGGCTGAGTA
priC	GCGCGTTAACCCGCTAG	GCGCGTTAACCCGCTAA	TTATTTCTCACTTTCCGCTCATC
aes-	CAGTTCTTACCGCTAGCTTAG	CAGTTCTTACCGCTAGCTTAA	ATTCAACAGTTAAAGTATGCGCTCC
ybcF	GGGACCTGTATTGCGCTGTAG	GGGACCTGTATTGCGCTGTAA	GTTCGTTAACTGGTGTCTATT
tra5	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTAA	TCCTAAAAAAATCAGATTGCGTCAC
ybcL	CTGAGATAACACCACTTATGAGATAAAGTAG	CTGAGATAACACCACTTATGAGATAAAGTAA	ATTATCAACAGTTAAAGTATGCGCTCC
rzpD	CAGAAGTATATTAAATGAGCAGTCAGATAG	CAGAAGTATATTAAATGAGCAGTCAGATAA	CGATGCAGCTAAATTGTGGC
ybcY	TAATGTTCCGCTCAGGAAAAAAATAG	TAATGTTCCGCTCAGGAAAAAAATAA	ACGGAGGAAGAACCTCATTG

hokE	CGCTTACGAACCGAAGAAGTAG	CGCTTACGAACCGAAGAAGTAGAA	CGGGCGGGTTAGAGC
ybdL	GCCTCGGCCAGCTTAG	GCCTCGGCCAGCTTAA	CGCCATCAAATACCGCC
ybdM	GCGCCTGGACGGTAAATAG	GCGCCTGGACGGTAAATAA	GCGGTTCTACCCTGGATGA
rIpA	GTCATTATTACTACCGCCAGTAG	GTCATTATTACTACCGCCAGTAGAA	GGCGCTTCATGATACTGAGC
ybeQ	AAATTCTGTGAGACTGAAGATTACTGTAG	AAATTCTGTGAGACTGAAGATTACTGTAA	GAGAAATGTCACTCCATCTCCC
ubiF	GCTGAAATATGCGTTAGGGTTGTAG	GCTGAAATATGCGTTAGGGTTGTAA	TCGAATCCTCGTACCCAG
ybfH	GAGGTCTGCTGATTGATAATGGTTAG	GAGGTCTGCTGATTGATAATGGTTAA	AAAATAATAACGCAGGCCAGTATCTTC
ybfD	GATGAGCTTATTGATTCACGTTGAATAG	GATGAGCTTATTGATTCACGTTGAATAA	TCATCAAATCGTTAGATTCAACTGC
nei-	CCTGGCTGCCAGCACTAG	CCTGGCTGCCAGCACTAA	TTTATGACTGCCTACCTCGCC
abrB	CGAACGGTCGGCCTAG	CGAACGGTCGGCCTAA	ACTGGAGATTCCCTCGATTTCT
sucB	TCTGCTGCTGGACGTGTAG	TCTGCTGCTGGACGTGTAA	GATAAGACACGTTAACGTCACATCA
bioD	AGTACATAAACCTGCCTGTTGTAG	AGTACATAAACCTGCCTGTTGTAA	AGGAATAGTGGATAACTGTCTCCAG
moaE	GCGGCAAAACGCTGGTAG	GCGGCAAAACGCTGGTA	CAGCCGGGGTTGTACG
ybhM	AAGGCATAACCGTTTTTCATTAG	AAGGCATAACCGTTTTTCATTAA	CCAAAGGTACAATTATGCCGC
ybhS	CCAAACGTGGCTGGATTAG	CCAAACGTGGCTGGATTAA	TTATCTTCATCGTAGATGGCGATG
ybiH	AAGGATTATCGCAAAGGAGTTGTAG	AAGGATTATCGCAAAGGAGTTGTAA	CCAGCGATTCAACGC
ybiR	TTAGTTACTCCCCGGCCAACTAG	TTAGTTACTCCCCGGCCAACTA	TGTCCAATTACCCGTACGA
yliD	CGCTGGATCCGAAAATTAAAGGATAG	CGCTGGATCCGAAAATTAAAGGATAA	AATACATTAAACAAAATAACTATCTGAACGCTG
yliE	TTGGATAAAAGTGGAAAATTAGAAAAGAGTAG	TTGGATAAAAGTGGAAAATTAGAAAAGAGTAA	CAGCAATATTGCCACCGCA
ybjK	TTGAGAGGGTTGCAGGGTAG	TTGAGAGGGTTGCAGGGTA	GGATAAAACTGAAGTTGCCCTGAA
rimK	GCCTGAAAACGGGTGGTAG	GCCTGAAAACGGGTGGTAGAA	AGCCTGACAGTTACATTCAAAAAA
ybjR	TGGAGAAATACGGGCAGGATTAG	TGGAGAAATACGGGCAGGATTAA	CCGCAAGTCAGCAAAAGAGC
cspD	GAAGCGGCAGTCGCATAG	GAAGCGGCAGTCGCATAA	TGGGAGATTGGTTTCACCG
lolA	TCACGGTAGATGATCAACGTAAGTAG	TCACGGTAGATGATCAACGTAAGTAA	AGGATCATAGAATGAAATGCCCG
ycaI	TGCCAGTGGATAACGGGTAG	TGCCAGTGGATAACGGGTAA	AAGGAGCGATAACATGAAGGTATC
lpxK	GCTGGCTTCTGGCAACTAG	GCTGGCTTCTGGCAACTAA	TGGTATCGATTGAGCAAGG
ycbK	CAGCACGGCACTGGTAG	CAGCACGGCACTGGTAA	GGATCTGCATCAGTGTCAAGG
ycbX	GCACTTAAGTTGGCGCGTTAG	GCACTTAAGTTGGCGCGTTAA	CACGAGCAGGTCAATTGCT
tra5	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTAA	TGTGACTCAGGAAAATGCGTTAAA
yceO	GCAATTATGGATCTGATCTATGTGTTTATTAG	GCAATTATGGATCTGATCTATGTGTTTATTAA	TTTCAATAATTGAAATTAAATAATGAAAGAATCTTCATAAGT
yceF	AAAAAACCCGCTGATGGGATAG	AAAAAACCCGCTGATGGGATAA	GCGTATCGAAGCTCCGATG
plsX	AGCGGAACCTCGCGTAG	AGCGGAACCTCGCGTAGAA	TACCGGTACGAGTGACAATCC
fabH	CGCGCTGGTCGTTCTAG	CGCGCTGGTCGTTCTAA	GTTCTTCAGCTGGCCCT
pabC	TTTGTGAGGCCCGAATTAG	TTTGTGAGGCCCGAATTAA	CGGCATAAAAGCTGTTACCG
b114	AGACCGGATATCTATCGAAAGATTAG	AGACCGGATATCTATCGAAAGATTAA	AAGCGTTCTGTTACATCGAGC
ymfM	AGTTTCGTCGAAATTCAAGGAAATAG	AGTTTCGTCGAAATTCAAGGAAATAA	CTCATCCCCGCGCCA
ymfR	TCTGTCGGCGGAGGTAAATAG	TCTGTCGGCGGAGGTAAATAA	CCCGACCGACTCTGCC
tfaE	AACTGCCGGAGGCGTAG	AACTGCCGGAGGCGTAGAA	CGAACCTTCAAAAGCAGATGCTTATC
ycgX	CTTTATATATTGAAGATGTAGAAAATAATAAACCATTAATCTAG	CTTTATATATTGAAGATGTAGAAAATAATAAACCATTA	CAAATATCAAGTTGATAGTATTAGTCTGGTGAT
ymgC	AGGAATCCGTCTCTTAG	AGGAATCCGTCTCTTAA	AATGTAGGCAGTACAAAATAAGTTAGGC
ycgY	GGACTGAAAACCGTCTGTGTAG	GGACTGAAAACCGTCTGTGTAA	CGAAAGAGCAACCGTGTGAC
hemA	GCCTCGGGCTGGAGTAG	GCCTCGGGCTGGAGTAA	CATCACTTAAC TGCGCATATTG

b122	GCTCGAGCCGAACCTAG	GCTCGAGCCGAACCTAA	TCGACCAAGGTTGACTCG
kch-sapB	CAGTAAAGAATCGCGCAAAAATAG	CAGTAAAGAATCGCGCAAAAATAA	CCGACGTAATCGCGTTGG
pspF	CATAAGGAATGGTATGCCTTACGATAG	CATAAGGAATGGTATGCCTTACGATAA	ATTGATAACCGAGAAAATTGCTGGTC
ycjU	CGTTGTTAAAAAGCACCAGATTAG	CGTTGTTAAAAGCACCAGATTAA	GGATGCGCAATTGATGC
ycjV	GGCCTTCTGGCAAAACGTATAAG	GGCCTTCTGGCAAAACGTATAA	CTCCTCAAGCCCGGCA
ycjG	GTTGGGGGCACGAGTTAG	GTTGGGGGCACGAGTTAA	CGGTACAGGTAATAACTTTTCATTATTG
ycjZ	ACGGGCGAATTGCATCTTAG	ACGGGCGAATTGCATCTTTAA	GGCTCAGGGCTTGAAATTG
intR	GGCTGAAGTATAAAGGTGCTGTTAG	GGCTGAAGTATAAAGGTGCTGTTAA	GTAAAGCACATAGAACCTCGAACAA
sieB	TTGAATGCGCGGTTATCGTAG	TTGAATGCGCGGTTATCGTAA	ATGATGCGATGCCCTCTTC
b135	GCAGGAGTAGACGTTTAATCGTTAG	GCAGGAGTAGACGTTTAATCGTAA	AACAAGATGTGAGATTGCAAATG
ydaY	GAATCTCACATCTGCTACGTATAG	GAATCTCACATCTGCTACGTATAA	GATTCAAATTGCACTGCAGCA
b136	AGCAGGATACGATAAAAAGCCATAG	AGCAGGATACGATAAAAAGCCATAA	CAGCATTCCAGCATAACGTC
tfaR	GTATTTCAGGAGCAGTGTGTAG	GTATTTCAGGAGCAGTGTGTAA	GCTCTGCCATTATAAAACTCCTGA
paaG	GCCAGCACTGCCGTAG	GCCAGCACTGCCGTAA	AGTATAAGTGCCTTGCCCCG
paaX	CGCAGTTACGGGGAAATAG	CGCAGTTACGGGGAAATAA	TTTCCC CGGTACCGC
b140	AGGCGTTATCCAATTTCAGATAG	AGGCGTTATGCCAATTTCAGATAA	GCATAACGCAATTATCCTGAATGTT
ydcL	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	GTATATCTGAATGGAGATACGACAATCAG
rhsE	CACCATGTTGACGTTAACAAAAGTAG	CACCATGTTGACGTTAACAAAAGTAA	GCTATTTGCCAGTAGCTGCG
yddJ	AGGGAGTTCAGATGCTTCAAATTATTAG	AGGGAGTTCAGATGCTTCAAATTATTAA	TTATAAAATGACCATTCCCTACTAATTTTTG
ddpF	CCTCCAGTTCATGGCTTTAG	CCTCCAGTTCATGGCTTTAA	GGGATTAAGTAGCCAGATATGTGTAC
yddV	TGGCGGGCGCTGTAG	TGGCGGGCGCTGTAA	GAGTGAAGTTGCGGTGCC
ydeV	GAACCTGGAAGCCAGTCTTAG	GAACCTGGAAGCCAGTCTTAA	TCTTCACGTTGTATCCCCAGA
ydeA	GGAAAGCGCCTGGTTATAG	GGAAAGCGCCTGGTTATAA	ATAAGGGTTGCTTAATGCTTAAAGA
marA	CACTCGAAGAACAGACGCAATAG	CACTCGAAGAACAGACGCAATAA	TGGGGAAAGCCTACGCA
marB	TTTTACATCATTAAATCATTACAACAGCTAG	TTTTACATCATTAAATCATTACAACAGCTAA	GTGGGTGTTCTCGATG
tfaQ	GCCCTATTATAATCAACACGCTATGTAG	GCCCTATTATAATCAACACGCTATGTAA	AGTAGGACTGGCAAGTGC
ydfP	GCCAGCACTGCCGTAG	GCCAGCACTGCCGTAA	AGTATAAGTGCCTTGCCCCG
rzpQ	TGAATCTTAAGAGATAAAAAGCATCAAATGTAG	TGAATCTTAAGAGATAAAAAGCATCAAATGTAA	AAAAAACACAGCAATGAAAGAATAGCT
b157	CAGAATGATTACATACCCCGTAG	CAGAATGATTACATACCCCGTTAA	GCTATATGAACCAAGCTACCTCG
ynfA	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	TCTTCAGTGCCTGAAATCTACG
speG	TGGGGCGCACGTAG	TGGGGCGCACGTAA	TGTCGTGATGCATGAAATCTACG
dmsD	GAAGCCGACCGCACAATAG	GAAGCCGACCGCACAATAA	AATTAGATTACACAGCGGTTACTTACTG
ydhM	CGGTTAACCGCTGTTCGATAG	CGGTTAACCGCTGTTCGATAA	AGATGTGTAGATGATGCATGAGCA
Ihr-	CGACGCCTGCCGTAG	CGACGCCTGCCGTAA	ACGTTGGCGATAGTATTCCG
ynhG	AAGGGCTGGATTGGGGATAG	AAGGGCTGGATTGGGGATAA	ACTGTGGGTTGACGGCG
sufA	GTTACGCGTGACGCAGTAG	GTTACGCGTGACGCAGTAA	AGTTGACCAGCTGAGCAAC
ydiA	GGCGAAAGCTTGGGTATAG	GGCGAAAGCTTGGGTATAA	CAGCATCCACTCCGGCT
ydiE	CCTTAGTCGCCGAATGTACTAG	CCTTAGTCGCCGAATGTACTAA	GGAGTTCGTCAGTTCTGTTATTAC
nlpC	CAAGCTGCTGTTGACCAAGTAG	CAAGCTGCTGTTGACCAAGTAA	GGTATTGCGCAACTGGTTGG
btuC	GGCAGGCAGACGAATCTAG	GGCAGGCAGACGAATCTAA	ACAATTACAGAAGGAGTAACCTTATTGT
arpB	TGGTTATTGTTAAAAGCAGGACGTTAG	TGGTTATTGTTAAAAGCAGGACGTTAA	ACACTTTGGCGACATTGAC
	CACCCAACAGTAAATCTCAATGGTAG	CACCCAACAGTAAATCTCAATGGTAA	GCTCTGAACCTCCCGTC

ydjX	ACTTACTCACCCAAAAAATGAAGGATAG	ACTTACTCACCCAAAAAATGAAGGATAA	CGTATGGTTATTGGCATCGACA
nudG	GCCAGACCAGCGGATTAG	GCCAGACCAGCGGATTAA	CCCGCATTATCGTCGGA
b178	ATCGAACGGACCGGCTAG	ATCGAACGGACCGGCTAA	GCGCGATCCCCCCTT
yeaL	GCTGATTGTGGGGAAACAGTAG	GCTGATTGTGGGGAAACAGTAG	TTGAGTTTCGCCAGTGGC
yeaX	CGCCTGGTGTGGATTGTAG	CGCCTGGTGTGGATTGTAA	AACCAACTGCTGAACCTGGC
yobB	GGCGATATCATTCCATTACGCTAG	GGCGATATCATTCCATTACGCTAA	ATGAATCGCCATCGCTTG
exoX	TTAACACTGAAACATTATCTGGAAAATACCTAG	TTAACACTGAAACATTATCTGGAAAATACCTAA	AATTGCGCGAGCTGAAAAC
yeN	GTTGGTTTCCTCCCTGCGTTAG	GTTGGTTTCCTCCCTGCGTTAA	AATCATGGAATAATATTGGAATAGCCGG
otsA	ACCTTCCAAGCTTGCCTAG	ACCTTCCAAGCTTGCCTAA	CCTACGGTGAGTTAAGCGAAC
dcyD	GCCTATCATCCCCACGTTAG	GCCTATCATCCCCACGTTAA	CACGAAAAATAGAGATATAAAACGCGC
yedM	CCCACCCATTGGCATAAATTAG	CCCACCCATTGGCATAAATTAA	TGTGGAGTTCAACACATTAAACAATC
fliE	GTGATGAGCATGCAGGTGTA	GTGATGAGCATGCAGGTGTA	ACGTGGTGTGCAAATGAG
fliN	GCGCCTGAGCCGTTAG	GCGCCTGAGCCGTTAA	AAGCACTGGCGCTAATTTC
fliP	GCGCAGAGCTTACAGCTAG	GCGCAGAGCTTACAGCTAA	GCGATGATTTCGAATAAACGAC
fliQ	CCTGCCGTATATCATGGGTAG	CCTGCCGTATATCATGGGTAA	TGATGGGCAATGGCGA
yedS	CGTAACAATGGCTCTTGGTTAG	CGTAACAATGGCTCTTGGTTAA	TATGCAGCACCCAGACTTAAAC
cbl-	GCAGTGAAGAGGAAATTGATTACAGATATAG	GCAGTGAAGAGGAAATTGATTACAGATATAA	AAAAATCGGGTTGACAAAAGATTTC
b199	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	CAACCTTGGGAAAGCCG
hisL	CCATCATCACCACATCCTGACTAG	CCATCATCACCACATCCTGACTAA	AGCTATGCGTAACCGAGTGTG
wbbJ	TGAGACCAAATTATGGGAAAAAGCATAG	TGAGACCAAATTATGGGAAAAAGCATAA	TTAACCTCAGGAAACTCAATGAATTAAACC
wcaM	GCCGGAACTGAGGGAGTAG	GCCGGAACTGAGGGAGTAA	TCGTCAATTTCATCCACCTGTAAAAT
wcaL	AGCTTGCTGCAGGCTTATAG	AGCTTGCTGCAGGCTTATAA	GCCCTTCGCTGAAGGC
wcaC	GAGTATGTCAACTTCTATCAGAATCTGTAG	GAGTATGTCAACTTCTATCAGAATCTGTAA	TGAGTCCC CGCGCAAT
asmA	GAAGAAGTTGCTGGAGAAGATGTAG	GAAGAAGTTGCTGGAGAAGATGTAA	AGATTGAGCCACCCCTGGC
baeR	GCCTGCCGCATCGTTAG	GCCTGCCGCATCGTTAA	CTTGATTGAAATTGTGTATCGAAAACAGC
gatR	CGCGGGTAAATTAAATTACGGTGTAG	CGCGGGTAAATTAAATTACGGTGTAA	GGCGAACCGTTGAGTGG
tra5	CAATTGAAAACAAGAACCTCGCTTAG	CAATTGAAAACAAGAACCTCGCTTAA	ACAAAAAGGCGTGGTTACGC
yegV	TCCTCGCACACAAAACGTATAG	TCCTCGCACACAAAACGTATAA	AGCCAGCACATTACCCACA
yegW	CGTTTTGTGTGCGAGGAGTAG	CGTTTTGTGTGCGAGGAGTAA	TCCGGCATTTCACACGC
yehQ	AGAGTGTATTGGTCAGGCATAG	AGAGTGTATTGGTCAGGCATAA	CTCTTAGAAAAGCACTATTTCATCCTT
yohC	GGCTACGGTTATCGTTGTTCTAG	GGCTACGGTTATCGTTGTTCTAA	CATGATGAGCATTAGATAGTGGTT
yohF	GAATCCACAGTTCAACCCAGAATAG	GAATCCACAGTTCAACCCAGAATAA	GTGGCTGAAACGACGCG
sanA	TTACTTGAATTACAAAAGAAACAAGGAAAGTAG	TTACTTGAATTACAAAAGAAACAAGGAAAGTAA	AAAAAAGAGTCCGGGATTTC
yejA	GCCAGCAAACAGGGAGAGTAG	GCCAGCAAACAGGGAGAGTAA	GCACGAACACCTTCACCG
yejE	CATTGATCCTAATAAGGCGGTGTAG	CATTGATCCTAATAAGGCGGTGTAA	AGGCCTAAAATTGACAGCGC
b219	GTAAATGCCCTGAATCAGCTATTAG	GTAAATGCCCTGAATCAGCTATTAA	CAAGCGACAGTCGGCTTC
rcsD	CAGTTATGTCAAGAGCTGCTGTAG	CAGTTATGTCAAGAGCTGCTGTAA	CAACACATGCGCATCCAGT
rcsC	GGAAATCGCGGGATTGTAG	GGAAATCGCGGGATTGTAA	GACCGCTTAGTGTCTTATCTGG
yfaT	CGTTTAAATTCTGGCGCGATAG	CGTTTAAATTCTGGCGCGATAA	CCGATAATCACGCCCG
menF	GCTCGTACTTATTACAAATGGAATAG	GCTCGTACTTATTACAAATGGAATAA	GATACAGATGTGTCTGACGCC
yfcO	GTTCCAGTACACTGAATGAGTTGTAG	GTTCCAGTACACTGAATGAGTTGTAA	CATGTGATGGCCTTTCATCAGG
yfcU	GGCGGATAAGGGCATGTAG	GGCGGATAAGGGCATGTAA	ATCATGGCTGTAGTAGCCATCAA

tfAS	CTGAAC TGCCGGAGGAGTAG	CTGAAC TGCCGGAGGAGTAGAA	AACTGAAAAAGCAGCAATTGATTAATCA
ypdI	CGAATTATCTTATTCATCCTGTGCGATAG	CGAATTATCTTATTCATCCTGTGCGATAA	CTGGCGGTAAATGAACTAGTGAC
yfdY	GGGTATGGCAGGCCTAG	GGGTATGGCAGGCCTAA	GATTTGTTAACATGAGAGAACATGCG
yfeO	CCACCCCACGATAACGTTAG	CCACCCCACGATAACGTTAA	CCTGCCTTGTCTGCAAG
mntH	ACGGCGCTGGGATTGTAG	ACGGCGCTGGGATTGTAA	GATCATCGCGAAAAGGCC
xapR	TTGGCTGCATTGACACAGTAG	TTGGCTGCATTGACACAGTAA	CGAAACAACGGAGGCCG
yfeR	AAGGGGATCCGTTGTATCAGATATAAG	AAGGGGATCCGTTGTATCAGATATAA	GAATGGCGCAGTTGCACT
yffB	TATCAGCAATTTCATGAGGTGTAG	TATCAGCAATTTCATGAGGTGTAA	CCCGGCAAAGGCTAACG
hda-	CGTTGTGAAAGAAATTCTGAAGTTGTAG	CGTTGTGAAAGAAATTCTGAAGTTGTAA	TCCACCGGAGCAGGTACT
yfgG	CGAATCACCGGTACAACGTTAG	CGAATCACCGGTACAACGTTAA	CATTACAACATATATATTAAATTATTTATTCAGGCC
pbpC	CGACAGTGAATTGTATGCAATAG	CGACAGTGAATTGTATGCAATAA	ATGGAAAAAGTACGTTCAATAGCCAT
yphA	CAATTCTCTCGATGGCGTTAG	CAATTCTCTCGATGGCGTTAA	TTCTCTGTCTGGAACCGATGA
yfhB	GTGAAC TCCAGCACTGGAATAG	GTGAAC TCCAGCACTGGAATAA	TACCCGATTGTTATGCACTAATACC
kgtP	GGAAAGGGATGCGTCTTAG	GGAAAGGGATGCGTCTTAA	GCATCAGGGATGAGCCG
yfIA	CGTCGAAGAAGTTGAAGAACAGTAG	CGTCGAAGAAGTTGAAGAACAGTAGAA	TTCACACGACGAAACGCC
yfjQ	GCTCACGCACTGCACTGAGTAG	GCTCACGCACTGCACTGAGTAA	CCAGGAAAGTTAACTGACTGAAAATGA
yfjR	CGACAGCCCCACCGGAATAG	CGACAGCCCCACCGGAATAA	ACTGGCAGCACCGGC
ypjC	GTTTTTGAATGCGCTAAAGAAATGAATAG	GTTTTTGAATGCGCTAAAGAAATGAATAA	GGTGTCTCTTGACTCTGACAAA
ygaQ	CAGACAGGATAGGAGAGAAAGAAAAACATAG	CAGACAGGATAGGAGAGAAAGAAAAACATAA	ATTATATACATCGGCTGCCAGCT
ygaR	AAGGTGGTATCCCTGGCTATTAG	AAGGTGGTATCCCTGGCTATTAA	AGGCATTCCATTAAACGCTTTTC
yqaC	CGGCGGTGAGGCCTAG	CGGCGGTGAGGCCTAA	TATTTATTATAACTAGCCATCATGAGGAGAGT
gabT	TTTGATGAGGCGAAGCAGTAG	TTTGATGAGGCGAAGCAGTAA	TCACCGTATAATTGTTATTGATTCTTTT
ygaU	GTTCGTATTCCCGGAAGAGTAG	GTTCGTATTCCCGGAAGAGTAA	ATTATCTGGCTGCCGGCG
ygaM	GTTAACATGCGCAAATCGTAG	GTTAACATGCGCAAATCGTAA	AGAGATACTAGATGTAGTTGAAAAAGATTCAA
luxS	GTTGCAGGAAC TGCACTCTAG	GTTGCAGGAAC TGCACTCTAA	TTCCGCCAATGAGATCTCTGG
mltB	GCTGGCGCGAGTACAGTAG	GCTGGCGCGAGTACAGTAA	CCTGTTCACTTAAC TGCACTCAGTT
srlE	GGTTTGTCCTCGGTTTATCTATCAATAG	GGTTTGTCCTCGGTTTATCTATCAATAA	GGATGGAGTGCACCTTCAAC
norW	GATTGTTAAAACATTGCCGATGTAG	GATTGTTAAAACATTGCCGATGTAA	TTATTGCTGCCGCCG
ascB	CCAGTAATGGGAAGATTAGAGTAG	CCAGTAATGGGAAGATTAGAGTAA	GGTGGAAAGAGAGTAGTTTCTTAAGG
hycI	AGTTAGCGGTGGAAGAACAGTAG	AGTTAGCGGTGGAAGAACAGTAG	TGGGAAAGATTAGAGTAGGTAACAG
hypB	GAGACACAGCGATGTGCA TAG	GAGACACAGCGATGTGCA TAGAA	TTCGGCTTCAATTACGCTCAT
ygbA	TATCGTCCGAAAAAACCTCATGAATAG	TATCGTCCGAAAAAACCTCATGAATAA	TGATTGTCGCGTGTCTG
pphB	GGCGGCTGTCATTTATAAAATAAGTAG	GGCGGCTGTCATTTATAAAATAAGTAA	ATGGCTGGCGTTACCATTAAGG
ygcN	AGGAGTCTCGCATGTCTGTAG	AGGAGTCTCGCATGTCTGTAA	CAGCAAACGGCAGGTGC
mazF	GCCAAAATTAAACGTACTGATTGGGTAG	GCCAAAATTAAACGTACTGATTGGGTAA	AAAGCGCAATGGTGGC
relA	TCGGTTGCACGGGAGTTAG	TCGGTTGCACGGGAGTTAA	ATCTTCACTTCATCATCAATATTGAGATTGA
rumA	GTACTTTCTCGCGCTAAATAG	GTACTTTCTCGCGCTAAATAA	CAGACAATACGCCAGGTTTC
ppdC	CATTGCCCGAATCGTCAGTAG	CATTGCCCGAATCGTCAGTAA	ATACCAAACTTGCGACAGGG
ptsP	CTGATT CGCGGAGGGTTATAG	CTGATT CGCGGAGGGTTATAA	TCCGGAAAATGCAGATAGCTACT
mutH	CCCGTCATTTCTGATCCAGTAG	CCCGTCATTTCTGATCCAGTAA	CCACCAAGAGAACAGGAAAATAATTGTC
ygeA	TGTCGCTTTATGCTGCGTAG	TGTCGCTTTATGCTGCGTAA	CTAGATTGCGGCAAGCGG
kduI	GGCGTTAAAGATTGCGCTAG	GGCGTTAAAGATTGCGCTAA	CTCGATGGTTCACTGCGTT

yqeF	TTGACCATTGAACGTGACGAATAG	TTGACCATTGAACGTGACGAATAA	CCATGGCTAGGGTTTCAATTAA
ypeI	CTATCTCACCTTACTATAAAATTGAGTGGTAG	CTATCTCACCTTACTATAAAATTGAGTGGTAG	GAGCAAGAGTTGCTGGCG
pbl-	CAAAATATATATTGTATATACCAGGCTTAATGAACTAG	CAAAATATATATTGTATATACCAGGCTTAATGAACTAA	GCAGTTAACGCAGGAAAACAGTCG
ypeM	GGCAAGGCCCTGAGGACTTATAG	GGCAAGGCCCTGAGGACTTATAA	TCATCCCTTCATTATTATAAGCAAATCC
b286	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	ATCGTGCCTTCTATTATTCAG
ypeP	ACACCAGAAGAAAAGAGCAAGTTAG	ACACCAGAAGAAAAGAGCAAGTTAA	CCCGGTTCAAAGCTCTGC
yqeC	GCGCGCAGATTGTGAATTAG	GCGCGCAGATTGTGAATTAA	GATAGAACCATCGGCCGCG
ygfJ	AGCGAAGGAAAGGTATACTGAAATTAG	AGCGAAGGAAAGGTATACTGAAATTAA	TTTGTGAATGAACTCACAGGTGC
recJ	TCATCGACAATATCTGGCCAATTAG	TCATCGACAATATCTGGCCAATTAA	TCGTAGTCAAAGATACCCCCTAAG
argO	TGCACAAGCCTTGTTCAGTTAG	TGCACAAGCCTTGTTCAGTTAA	TGCGGTCCATCCGGC
yggU	CAGAAATCGCGCGTTATTAAATTAG	CAGAAATCGCGCGTTATTAAATTAA	TGGCGCGCTTCAGAACATC
mutY	GGCGCGCCGGTTAG	GGCGCGCCGGTTAA	TTTCATTAATCAGCATGGTTTGCTTG
glcC	GCTGGAGATGAACCTGAGTTAG	GCTGGAGATGAACCTGAGTTAA	GGTATTGCGCTTTATTGATTG
yghQ	CTCGAAGCGTATGACCTGATTAG	CTCGAAGCGTATGACCTGATTAA	ATGATACGTCACTGGGAGAGATC
yghT	CGCGCGTGGTTACTAG	CGCGCGTGGTTACTAA	GACGATGGTGGTGGACGG
ygiZ	TGGGGACGGTTATATTTGCTATTAG	TGGGGACGGTTATATTTGCTATTAA	CCGGACAAACCGCTACC
yqiB	CGATGGCGATTCCGGTTATTAG	CGATGGCGATTCCGGTTATTAA	TGGCCGAATCGCCCTCC
b304	GGTTAAGTGATAACAGATGTCTGGAAATATAG	GGTTAAGTGATAACAGATGTCTGGAAATATAA	TCTTATTATTAATCAGAGTGCCTAGTGAATATTG
yqiI	GACGTAATCCTGAAAATCACCTATAACTAG	GACGTAATCCTGAAAATCACCTATAACTAA	GTCGCCCGGTCGATATTCT
ygiP	GATGAAGGCTATCAGGTATGTAG	GATGAAGGCTATCAGGTATGTAA	CGTTTATGTCGTTGGTTAAC
yhaK	CTTGCTGATAGATTGCTGTCTAG	CTTGCTGATAGATTGCTGTCTAA	TCATCCTCGGCTAACCGCG
tdcA	ACGAAGGCAATTAAATAGAAGTTGGTAG	ACGAAGGCAATTAAATAGAAGTTGGTAG	ATTCGCCAGCCAGTCG
yhaC	CGTATGATTACGACCTTTAAATGCAATATAG	CGTATGATTACGACCTTTAAATGCAATATAA	CAATATATTGCAAGAGTGGCGTAGG
ecfH	GTAACTACGGCGTTACGTTTAAATAAATAG	GTAACTACGGCGTTACGTTTAAATAAATAA	GGGGCGATGGTGGCA
yhbW	GATGTTAAGGAAGAGTTGGGATAG	GATGTTAAGGAAGAGTTGGGATAA	GCAACGCAGTGGTCATAT
nlpI	GCAGAACCGGACAGCAATAG	GCAGAACCGGACAGCAATAA	GTAGTACGTGTCCTAAATTAAATG
dacB	GCCGTTTGATAAAGATATTATCAGAACAAATTAG	GCCGTTGTATAAAGATATTATCAGAACAAATTAA	ATCAGCCTGATGCGCTACG
ptsN	GGTACTCCGGATGAAGCGTAG	GGTACTCCGGATGAAGCGTAG	GCCAGGGTTCGAGCCA
yhcC	GGCTACCTCCAACGGAGTAG	GGCTACCTCCAACGGAGTAA	GCGCCAGCAACATTGAGA
yhcE	GTAAATGCCTTGAATCAGCCTATTAG	GTAAATGCCTTGAATCAGCCTATTAA	CAAGCGACAGTCGGCTTC
yhcO	CATTGCGTTTAAATGTCGTCATTAG	CATTGCGTTTAAATGTCGTCATTAA	AATGGATATGCGTAAATGCTGAA
mreC	CGCCGGGAGGGCAATAG	CGCCGGGAGGGCAATAA	TCACAAAACCTGTGCCAC
yhdN	GTTGTTGGACAAAATCAACGATAACTAG	GTTGTTGGACAAAATCAACGATAACTAA	GGCATGGCGATAAATTCAATC
kefB	CGGCTGGGATGAATTGAGTAG	CGGCTGGGATGAATTGAGTAA	CATCTTGCAGCGTACG
frID	ACCACGGTGCCTGGTAG	ACCACGGTGCCTGGTAA	AAACCCCTGCGCGATAT
bioH	CGTTGAAGCAGAGGGTAG	CGTTGAAGCAGAGGGTAGAA	TAATGACTATTGCGGAAAGATTGCG
gntX	GTGCCTTGTGAACCTTGTAG	GTGCCTTGTGAACCTTGTAA	GCCACATTCAAGCGTTAGGC
malQ	GCTGCAGCGAAGAAGAAGTAG	GCTGCAGCGAAGAAGAAGTAA	TCGATGCTGGAAACCATTATCTC
glgA	CGTGAGCTTACTATCGCTTGAATAG	CGTGAGCTTACTATCGCTTGAATAA	CGATCGCGCACAGCAAATA
yrhA	TGATGCTGCCAACTTACTGATTAG	TGATGCTGCCAACTTACTGATTAA	TTGAGAAGCGGTGAAAGTGAAC
ugpQ	CCGAACTTACGGCCAATAG	CCGAACTTACGGCCAATAA	ATAATTCTCAGCGGGTGTG
gadE	CACCCCTGGGTATCACATCTTATTAG	CACCCCTGGGTATCACATCTTATTAA	TCTGCCAACAGTTCTGCC

gadX	CGTTCTCGGAAGGAATAAGATTATAG	CGTTCTCGGAAGGAATAAGATTATAA	GTTTATAAAAAAATGGCTGATCTATTCAGTA
yhjK	GAAGAGAGTACCTGGAAGAAAAGTAG	GAAGAGAGTACCTGGAAGAAAAGTAG	TTTAGTAAACACAGGTCTTGAAGG
yhjR	CAGAGTTGCGCAACAAAAGTAG	CAGAGTTGCGCAACAAAAGTAG	GACGGTGGGAAATCAACATTAATG
yiaG	GCATTAAGTAAGCAGTTGATGGAATAG	GCATTAAGTAAGCAGTTGATGGAATAA	TTGAAGGGACTTGCCTTACTACA
xylR	GATGTAATAGCGAGGTATGTTGAA	GATGTAATAGCGAGGTATGTTGAA	CGACTTGTCACTGGATAAGG
sgbU	GCAGGAGGCTGGATTATATGTTAG	GCAGGAGGCTGGATTATATGTTAA	ATCTCAACCACCACCATATCGT
rhsA	CCAGACAGTCAAACGATAAAAAAAGATAG	CCAGACAGTCAAACGATAAAAAAAGATAA	CTCTTAACGTAAACTCTGGCAGATG
yibA	GCTATTGATAAGCTGAAGCGTTCATAG	GCTATTGATAAGCTGAAGCGTTCATAA	CGGCGTGTACACCGG
lctD	CGAAAGGGATGCGGCATAG	CGAAAGGGATGCGGCATAA	GGGGCAGGATAGCAGAAAATTG
yibK	CGGGAGCGGTATTGAGAGATTAG	CGGGAGCGGTATTGAGAGATTAA	ATACCACCGCCGCTGG
yibD	TAGCGCCTTAATTGCGCTAG	TAGCGCCTTAATTGCGCTAA	CCGCGTAATCCGTTCCG
htrL	CGCTGAGAATTTCCTTCAGAAAATAG	CGCTGAGAATTTCCTTCAGAAAATAA	TGTAACTTGATGTCCTCAACACCTA
coaD	CTGATGGCGAAGTTAGCGTAG	CTGATGGCGAAGTTAGCGTAA	GATGGTAAACCGGGCTATTG
rph-	GAGGGGAATCGAACCTATTGAG	GAGGGGAATCGAACCTATTGAG	CCGGATTTCAGCGTAAACTCG
dinD	GGAAAACAGTGTAAAAATTACAGAGAAGAAATAG	GGAAAACAGTGTAAAAATTACAGAGAAGAAATAA	AGAGATGCATTCTTGACTTTG
ligB	GCAGATCACAGGTTTGAACCTTAG	GCAGATCACAGGTTTGAACCTTAA	AGTTGTATGCCGGTGTCTCA
setC	ATGATTGCCCTGCTGTTATTAAAGATATTAG	ATGATTGCCCTGCTGTTATTAAAGATATTAA	TCCCCACAACACGGCG
yicO	GCACTGAAGATTATTCTGGTGGATTAG	GCACTGAAGATTATTCTGGTGGATTAA	GTACGACATCGATGTTAGCC
ivbL	CGGCAATGCCCGTAG	CGGCAATGCCCGTAA	CCTGCTGTTCCAGGAAATGAAC
yidH	CTGGTGTGTTATGCCGGATAG	CTGGTGTGTTATGCCGGATAA	GGATCAGCGCCACGATG
glvC	GGCGGAGGTCTGATTGACTAG	GGCGGAGGTCTGATTGACTAA	GCTTTGAGTAGAGTTCACTCCG
yidS	GCACATATCCACAGTTGAAGGATTAG	GCACATATCCACAGTTGAAGGATTAA	TAACCGGCGGCGTGT
yieH	GTGGTTGGGATATTACGGCATAG	GTGGTTGGGATATTACGGCATAA	CAGCGTTCTTGCAGAAGA
yieJ	GACTGTGGGGTGTATTCGTAG	GACTGTGGGGTGTATTCGTAA	AAAATTTCTGCAAGGTCCGG
atpE	GATGTTCGCTGTCGCGTAG	GATGTTCGCTGTCGCGTAA	AATTCTTTGACGTTTCGATGGC

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